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day of January 1999

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MANAGER EXAMINATION SUPPORT AND SALES

AUSTRALIA

Patents Act 1990

CSL LIMITED

PROVISIONAL SPECIFICATION

Invention Title:

P. gingivalis antigens

The invention is described in the following statement:

M103455 04AUG98

P. gingivalis antigens

FIELD OF THE INVENTION

The present invention relates to *P. gingivalis* nucleotide sequences, *P. gingivalis* polypeptides and probes for detection of *P. gingivalis*.

BACKGROUND OF THE INVENTION

Periodontal diseases are bacterial-associated inflammatory diseases of the supporting tissues of the teeth and range from the relatively mild form of gingivitis, the non-specific, reversible inflammation of gingival tissue to the more aggressive forms of periodontitis which are characterised by the destruction of the tooth's supporting structures. Periodontitis is associated with a subgingival infection of a consortium of specific Gram-negative bacteria that leads to the destruction of the periodontium and is a major public health problem. One bacterium that has attracted considerable interest is *P. gingivalis* as the recovery of this microorganism from adult periodontitis lesions can be up to 50% of the subgingival anaerobically cultivable flora, whereas *P. gingivalis* is rarely recovered, and then in low numbers, from healthy sites. A proportional increase in the level of *P. gingivalis* in subgingival plaque has been associated with an increased severity of periodontitis and eradication of the microorganism from the cultivable subgingival microbial population is accompanied by resolution of the disease. The progression of periodontitis lesions in non-human primates has been demonstrated with the subgingival implantation of *P. gingivalis*. These findings in both animals and humans suggest a major role for *P. gingivalis* in the development of adult periodontitis.

P. gingivalis is a black-pigmented, anaerobic, asaccharolytic, proteolytic Gram-negative rod that obtains energy from the metabolism of specific amino acids. The microorganism has an absolute growth requirement for iron, preferentially in the form of haeme or its Fe(III) oxidation product haemin and when grown under conditions of excess haemin is highly virulent in experimental animals. A number of virulence factors have been implicated in the pathogenicity of *P. gingivalis* including the capsule, adhesins, cytotoxins and extracellular hydrolytic enzymes.

In order to develop an efficacious and safe vaccine to prevent *P. gingivalis* colonisation it is necessary to identify and produce antigens that are involved in virulence that have utility as immunogens to generate neutralising antibodies. Whilst it is possible to attempt to isolate antigens directly from cultures of *P. gingivalis* this is often difficult. For example as mentioned above, *P. gingivalis* is a strict anaerobe and can be difficult to isolate and grow. It is also known that, for a number of organisms, when cultured *in vitro* that many virulence genes are down regulated and the encoded proteins are no longer expressed. If conventional chemistry techniques were applied to purify vaccine candidates potentially important (protective) molecules may not be identified. With DNA sequencing, as the gene is present (but not transcribed) even when the organism is grown in vitro it can be identified, cloned and produced as a recombinant DNA protein. Similarly, a protective antigen or therapeutic target may be transiently expressed by the organism *in vitro* or produced in low levels making the identification of these molecules extremely difficult by conventional methods.

With serological identification of therapeutic targets one is limited to those responses which are detectable using standard methods such as Western Blotting or ELISA. The limitation here is the both the level of response that is generated by the animal or human and determining whether this response is protective, damaging or irrelevant. No such limitation is present with a sequencing approach to the identification of potential therapeutic or prophylactic targets.

It is also well known that *P. gingivalis* produces a range of broadly active proteases (University of Melbourne International Patent Application No PCT /AU 96/00673, US Patent Nos 5,475,097 and 5,523,390), which make the identification of intact proteins difficult because of their degradation by these proteases.

SUMMARY OF THE INVENTION

The present inventors have attempted to isolate *P. gingivalis* nucleotide sequences which can be used for recombinant production of *P. gingivalis* polypeptides and to develop nucleotide probes specific for *P. gingivalis*. The DNA sequences listed below have been selected from a large number of *P. gingivalis* sequences according to their indicative potential as vaccine candidates. This intuitive step involved comparison of the deduced protein sequence from the *P. gingivalis* DNA sequences to the known protein sequence databases. Some of the characteristics used to select useful vaccine candidates include; the expected cellular location, such as outer membrane proteins or secreted proteins, particular functional activities of similar proteins such as those with an enzymatic or proteolytic activity, proteins involved in essential metabolic pathways that when inactivated or blocked may be deleterious or lethal to the organism, proteins that might be expected to play a role in the pathogenesis of the organism eg. red cell lysis, cell agglutination or cell receptors and proteins which are paralogues to proteins with proven vaccine efficacy. DNA sequences that were considered to be poor vaccine candidates and not selected include those that code for proteins involved in replication, non-essential proteins involved in cellular processes and those proteins present at sites that would be unlikely to be affected by immune mediators such as those found in the bacterial cytoplasm or inner membranes.

In a first aspect the present invention consists in an isolated *P. gingivalis* nucleotide sequence, the nucleotide sequence consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1 to 44, fragments thereof and sequences complementary thereto.

In a second aspect the present invention consists in an isolated *P. gingivalis* polypeptide, the polypeptide being at least partially encoded by a nucleotide consisting of or including a sequence selected from the group consisting of SEQ ID NO: 1 to 44, fragments thereof and sequences complementary thereto.

In a third aspect the present invention consists in an isolated *P. gingivalis* polypeptide consisting of or including an amino acid sequence selected from the group consisting of SEQ ID NO: 45 to 137 or fragments thereof.

In a fourth aspect the present invention consists in an isolated polynucleotide, the polynucleotide encoding a polypeptide consisting of or including an amino acid sequence selected from the group consisting of SEQ ID NO: 45 to 137 or fragments thereof.

In a fourth aspect the present invention consists in a nucleotide probe specific for *P. gingivalis,* the probe including a detectable label and a nucleotide sequence of at least 15 nucleotides, the nucleotide sequence being derived from a sequence selected from the group consisting SEQ ID NO: 1 to 44 and sequences complementary thereto.

In a fifth aspect the present invention consists in a composition for use in raising an immune response in an animal directed against *P. gingivalis* the composition including an acceptable carrier and/or adjuvant and at least one polypeptide having a sequence selected from the group consisting of SEQ ID NO: 45 to 137 or fragments thereof.

As will be understood by those skilled in the art the nucleotides of the present invention may be useful in DNA vaccination to reduce the incidence and/or severity of *P. gingivalis* infection.

Accordingly in a sixth aspect the present invention consists in a composition for use in inducing an immune response, the composition including at least one DNA molecule, the at least one DNA molecule having or including a sequence selected from the group consisting of SEQ ID NO: 1 to 44, fragments thereof and sequences complementary thereto.

Further information regarding DNA vaccination may be found in Donnelly *et al*, Journal of Immunological Methods 176(1994) 145-152, the disclosure of which is incorporated herein by reference.

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

DETAILED DESCRIPTION

Preparation of the *P. gingivalis* library for sequencing.

To determine the DNA sequence of *P. gingivalis* genomic DNA was isolated from *P. gingivalis* strain W50 (ATCC 53978) essentially by the method described by Mamur J. (1961)(1). Cloning of DNA fragments was performed essentially as described by Fleischmann *et al.*, (1995)(2). Briefly, purified genomic DNA from *P. gingivalis* was nebulized to fragment the DNA and was treated with Bal31 nuclease to create blunt ends then run twice on preparative 1% agarose gels. DNA fragments of 1.6-2.0 kb were excised from the gel and the DNA recovered. This DNA was then ligated to the vector pUC18 (*Sma*I digested and dephosphorylated; Pharmacia) and electrophoresed on a 1% agarose preparative gel. The fragment comprising linear vector plus one insert was excised, purified and this process repeated to reduce any vector without insert contamination. The recovered vector plus insert DNA was blunt-ended with T4 DNA polymerase, then a final ligation to produce circular DNA was performed. Aliquots of Epicurian Coli Electroporation-Competent Cells (Stratagene) were transformed with the library DNA and plated out on SOB agar antibiotic diffusion plates containing X-gal and incubated at 37°C overnight. Colonies with inserts appeared white and those without inserts (vector alone) appeared blue. Plates were stored at 4°C until the white clones were picked and expanded for the extraction of plasmid DNA for sequencing.

DNA sequencing

Plasmid DNA was prepared by picking bacterial colonies into 1.5ml of LB, TB or SOB broth supplemented with 50-100ug/ml Ampicillin in 96 deep well plates. Plasmid DNA was isolated using the QIAprep Spin or QIAprep 96 Turbo miniprep kits (QIAGEN GmbH, Germany). DNA was eluted into a 96 well gridded array and stored at -20C.

Sequencing reactions were performed using ABI PRISM Dye Terminator and ABI PRISM BIGDye Terminator Cycle Sequencing Ready Reaction kits with AmpliTaq DNA polymerase FS (PE Applied Biosystems, Foster City, CA) using the M13 Universal forward and reverse sequencing primers. Sequence reactions were conducted on either a Perkin-Elmer GeneAmp 9700 (PE Applied Biosystems) or Hybaid PCR Express (Hybaid, UK) thermal cyclers. Sequencing reactions were analysed on ABI PRISM 377 DNA sequencers (PE Appled Biosystems). Raw trace data files from the ABI 377 sequencer were manually trimmed using Staden Pregap (Laboratory of Molecular Biology, Medical Research Council, UK) running on a Sun Microsystem computer. Trimmed files were assembled into contigs using Staden Gap v4.1 and exported as FastA consensus files.

DNA sequence data was supplemented with sequence downloaded from the Internet site of the Institute for Genome Research (http://www.tigr.org).

DNA sequence analysis

DNA files in FastA format were converted to GCG format files before translation into amino acid files using the program Flip obtained from ANGIS (Australian Genomic Information Service, University of Sydney, Australia). FastA homology searching and/or PSORT analysis(4,6) were used as data mining tool to select potential vaccine candidates. All proteins with a PSORT probability of outer membrane >0.8 were selected. The FastA results for these proteins were then examined for any alignment with a protein suggesting surface location of vaccine efficacy.

All proteins were searched for homology against a non-redundant Bacterial protein database compiled byANGIS using the FastA algorithm. The settings used for the FastA searches were Ktup = 2, gap creation penalty = -12, gap extension penalty = -2, width for deriving alignment in opt = 16 and the Blosum 50 scoring matrix. Individual FastA search results were examined for significant homology by statistical probability and amino acid alignments.

The results are set out in Table 1.

Protein files were then trimmed to the first, second and third methionine residues using a protein trimming program (ANGIS). The trimmed proteins were then subjected to PSORT analysis (4, 6) for the detection of signal sequences and the prediction of protein cell location.

The results are set out in Table 2.

The sequences obtained are set out below. The relationship between these sequences is set out in Table 3. The initiation codon was calculated using a combination of sequence homology alignment (FastA), signal sequence prediction (PSORT) or ORF prediction (GeneMark) (3).

As will be understood by those skilled in the art open reading frames (ORFs) may be readily identified. ORFs may be determined using three methods, for example, alignments from FastA search results may be used to define the start and end positions of coding regions if sufficient protein homology is present. Alternatively, protein coding regions may be identified using the ORF identification program GeneMark (3) using a matrix trained on published *P. gingivalis* sequences. This matrix may be further refined by adding ORFs identified from the results of homology searching and ORFs identified by GeneMark. Otherwise, the program PSORT (4,6) may be used for the detection of signal sequences at the start of a protein and the prediction of cell localisation. A UNIX version of TopPred (5) may also be used to identify potential membrane spanning domains.

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Dated this fourth day of August 1998

CSL LIMITED
Patent Attorneys for the Applicant:

F B RICE & CO

References.

1. Mamur, J. (1961) A procedure for the isolation of deoxyribonucleic acid from micro-organisms. J. Mol. Biol. 3, 208-218.

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4. Horton, P. and Nakai, K. (1996). A probabilistic classification system for predicting the cellular localization sites of proteins. Intellig. Syst. Mol. Biol. 4: 109-115.

5. Claros MG and G von Heijne. (1994). TopPred II: an improved software for membrane protein structure predictions. Comput. Appl. Biosci. 10: 685-686.

6. Nakai K, Kanehisa M. 1991. Expert systems for predicting protein localization sites in Gram-negative bacteria. Proteins: Structure, Function, and Genetics 11:95-110.

Table 1 Results of FastA homology searching

SeqID#	Length of ORF in SeqID	Homology description	Length of homolog	% identity	Overlap (aa)	E value
45	589aa	Fimbrilin ORF3, *Porphyromonas gingivalis*	670	46	592	2.30E-99
46	907aa	Gliding motility protein (gldA), *Flavobacterium johnsoniae*	578	23	572	7.90E-25
50	566aa	Outer membrane protein 11, *Helicobacter pylori*	186	25	183	2.00E+00
51	819aa	Ferric pseudobactin M114 receptor protein, *Pseudomonas* sp.	826	22	585	1.00E-05
58	973aa	Histidine kinase, *Pseudomonas putida*	978	28	554	4.80E-28
61	1162aa	Arginyl endopeptidase precursor, *Porphyromonas gingivalis*	991	24	328	7.30E-08
62	406aa	Outer membrane porin (porB), *Neisseria meningitidis*	332	23	239	4.50E-01
64	467aa	Component of alkaline protease secretion (aprF), *Pseudomonas aeruginosa*	481	21	427	3.40E-06
65	436aa	Outer membrane protein alkL, *Pseudomonas oleovorans*	230	26	136	2.70E+00
66	945aa	Gliding motility protein (gldA), *Flavobacterium johnsoniae*	578	21	639	7.30E-09
71	563aa	Neuraminidase precursor (nanH), *Bacteroides fragilis*	544	23	251	1.50E+00
75	211aa	Attachment and invasion protein homolog (ail), *Salmonella typhimurium*	165	21	140	1.90E+00
77	953aa	Conserved hypothetical secreted protein (HP1216), *Helicobacter pylori*	660	20	483	4.10E-04
79	962aa	Protease I (API) gene, *Achromobacter lyticus*	653	24	695	1.80E-22
80	1312aa	Cysteine protease, *Porphyromonas gingivalis*	364-2628	25	212	0.00011
81	938aa	Cysteine protease hagD, *Porphyromonas gingivalis*	989-2628	31	742	1.40E-23

Table 1 Results of FastA homology searching

SeqID#	Length of ORF in SeqID	Homology description	Length of homolog	% identity	Overlap (aa)	E value
82	1251aa	Serum opacity factor, *Streptococcus pyogenes*	1025	24	176	2.10E-01
83	426aa	Vacuolating cytotoxin gene (vacA), *Helicobacter pylori*	160	32	111	1.60E+00
85	266aa	Outer membnrane protein, *Neisseria gonorrhea*	174	22	153	6.60E+00
87	814aa	P1 cytoadherence protein, *Mycoplasma pneumoniae*	219	41	63	6.80E-01
88	451aa	TolC, *Salmonella enteritidis*	491	23	436	5.70E-11

Table 2 Results of protein analysis using Psort.
The type of signal sequence and the amino acid number of the most C-terminal residue of the signal sequence is listed. The abbreviations for cell location used in the table are: OM = outer membrane, IM = inner membrane, PS = periplasmic space.
The terminal amino acid may indicate surface location if it is an aromatic amino acid (F or Y).
* indicates an uncleavable signal sequence is present.
** indicates a lipoprotein signal sequence is present

Seq ID#	Signal present (Y/N)	Cleavage site	Cell location and probability			Terminal amino acid
			OM	IM	PS	
89	Y	20	0.94	0	0.31	N
90, 91	Y	20/24	O.82	0	0.19	F
92	Y	41	0.93	0	0.25	F
93, 94	Y	21/20	0.85	0	0.44	K
95	Y	28	0.93	0	0.25	F
96	Y	21	0.94	0	0.29	F
97	Y	32	0.93	0	0.26	G
98	Y	19	0.93	0	0.22	N
99	Y	27	0.94	0	0.32	H
100	Y	20	0.94	0	0.3	L
101	Y	21	0.93	0	0.24	F
102	Y	20	0.93	0	0.24	F
103	Y**	19	0.79	0.87	0	V
104	Y	24	0.94	0	0.32	L
60	Y	20	0.93	0	0.21	Q
105	Y	28	0.8	0	0.25	Q
106	Y	26	0.94	0	0.3	H
107	Y	20	0.93	0	0.19	F

Table 2 (cont.)

Seq ID#	Signal present (Y/N)	Cleavage site	Cell location and probability			Terminal amino acid
			OM	IM	PS	
108	Y	21*	0	0.18	0	F
109	Y	24	0.93	0	0.2	N
110	Y	57	0.93	0	0.21	S
111	Y	47	0.89	0	0.21	N
112	Y	22	0.94	0	0.32	V
113	Y	28	0.94	0	0.38	K
114	Y	18	0.93	0	0.25	F
115	Y	23	0.85	0	0.30	E
116	Y	25	0.88	0	0.35	N
117, 118	Y	19/18	0.89	0	0.25	P
119, 120	Y	25/23	0.93	0	0.25	N
121	Y	21	0.94	0	0.3	F
122	Y	19	0.85	0	0.3	R
123	Y	36	0.93	0	0.27	Y
124	Y	20	0.93	0	0.46	L
125	Y	20	0.86	0	0.25	Q
126	Y	21*	0	0.04	0	K
127, 128, 129	Y	24/20/21	0.53	0	0.2	P
130, 131	Y	25/24	0.91	0	0.31	Y
132	Y	29	0.93	0	0.21	F
133	Y	46	0.91	0	0.03	H
134	Y	24	0.93	0	0.24	F
135	Y	23	0.94	0	0.29	D
136	Y	25	0.85	0	0.37	R
137	Y	17	0.36	0	0.22	D

Table 3: Relationship between DNA and protein SeqID numbers

DNA sequence	ORF untrimmed	ORF trimmed to 1st Met	ORF trimmed to 2nd Met	ORF trimmed to 3rd Met
1	45			
2	46		89	
3	47	90	91	
4	48			92
5	49	93	94	
6	50	95		
7	51		96	
8	52	97		
9	53	98		
10	54	99		
11	55		100	
12	56	101		
13	57	102		
14	58	103		
15	59	104		
16	60			
17	61	105		
18	62	106		
19	63	107		
20	64	108		
21	65	109		
22	66	110		
23	67	111		
24	68	112		
25	69		113	
26	70	114		
27	71	115		
28	72		116	
29	73		117	118
30	74	119	120	
31	75	121		
32	76		122	
33	77	123		
34	78	124		
35	79	125		
36	80	126		
37	81	127	128	129
38	82	130	131	
39	83	132		
40	84	133		

Table 3 (cont.)

DNA sequence	ORF untrimmed	ORF trimmed to 1st Met	ORF trimmed to 2nd Met	ORF trimmed to 3rd Met
41	85	134		
42	86	135		
43	87	136		
44	88	137		

(2) INFORMATION FOR SEQ ID NO:1

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1768 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

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agactatcaa atccatgaag gggcctatat cattccggtc aaagagcaaa tgcgaccact     60
attcaatggc aacaacaact tcagcatcta tgtagtggcc aatctcgatt tcaatgctcc    120
ggccacagaa gctgcgcttt ctcaatttgt ggtagagaaa tctattgaag tctcttctac    180
gacagcccct gccgatttcg taatgcttgc tcatggcaat aagcagatca atatggctac    240
gacagaaggg aaactgttgg gggattataa actcaaacga gtggcagcaa agattcgcat    300
gataaaaccc accatcaatg tgcaaggata tgaagtggtc ggaaatatac aggcaaagtt    360
tcgcaattcg gtaacgaagg ggttccttac cacagaagct caagagatcc cagctgctgc    420
atcctataag acatcggaat atcttgatat tgcagagtcg gcacctgcca attctatcca    480
tttctattct tactataaca aatggacact ctccacaccg gagaagcgac cggaattctt    540
catcatggtc aaattcaaaa agacaggaca gccggacaac acagccaaac cgtactacta    600
cagagtgccc ctcgaatctc aggacaatca ggtcaagagc aatgtcctct ataatctgaa    660
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tgtgaaaatc gaaatcttgg gttctttaca agagccggaa gctgtttctg taaacggcac      720
actcgcaata gaagaatgga ttctccatca ggatgcattc aatctgcctg ccaccaatta      780
cttgatagtg gaacagcacg aaatcttcat gaataacgtg aacacatact cggtgaaata      840
tcaaacttcg cagaaaccaa tcagcattag catacagtca gttaccttta gctacgtctc      900
ttctgatggc actcagcaca atgatcttgt agcaagtagt agcgaccagt atcctacgat      960
tacaagcgat aatacaagca tcataatcac ttccaagata ccggttaata acgtaccaaa     1020
gaagatcgtt tttgaggtaa ctaatggggt agccggtttg aaagagactg tcacagtact     1080
ccaatatcct gcacaattta ttgtcaatac acttggcaca gcatcggcat ggagaccaga     1140
cggatctttg gctccggggc ttaacaataa agcgatttac catgtcgtag tactggttcc     1200
acccgagaat ttatttgaag atgggacaca gacaatcatc ggttatcccc ccactgaaac     1260
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gacaaaacag gaccttgaga catcaagaat gatttcacct tcctttgagt tagcctccca     1380
acttggggct actctcccga tgccctatct cgagtattgg ccagggacat catatctcct     1440
tgactattcg ggaaactata ataataagag atacgccttg tttaattgcg ctttttactg     1500
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agctgagatc aaattgatag ataagctgca acataatgag cagagtgctg tccaagctat     1620
catgacaggg aattattatt gggatagtta ctctgcaaat gggtcttata aaatgcaagg     1680
aggagggggc caaggaaatt cctccaaagc ctatgttcgt tgcgtgcggg atgtgaaaaa     1740
gccgattcgt gacaagaagt caggtaag                                        1768
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(2) INFORMATION FOR SEQ ID NO:2

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 2721 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Porphyromonas gingivalis*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

```
ACTATATGCG TTGCCTTCTT ATCCGCTCCC GTTGCGGCAT TGCGCGAGTC GCCGCCAATG     60
GGGGCGGAGC GGAAGACTCC CTCTCTCCTA CCCCTTCTTT TCGAGCATTC TGATAAAGGA    120
AAGGGGTTCG ACTACAGACT ATTCACAAGC AATAAACTTA AAGTGTTTGC CACAGGTAAC    180
AGCCGATACA TACACAATAA ACCAACAATC ATCCAAGCAA TGAAACGAAT CGTTTTATCA    240
TCTTTCCTGT TCGTTCTGTC CATACTTTCT TTGATGGCAC AGAACAATAC CCTCGATGTA    300
CACATATCCG GTACGATCAA GGATGCCTCC TCCGGCGAAC CAGTGCCCTA TGCCACTGTA    360
AGCATCCGGC TGACAGGAGC AGATACCACA CAGGTGTTCC GACAAGTGAC TGACGGCAAC    420
GGCTACTTCG TCATAGGCCT GCCGGCAGCT CCCTCCTATC ACCTGACAGC TTCGTTCGTA    480
GGTATGAAAA CCCATACCAT GCAGATTAGT CGGGGAAATG GACAGCACGA CATCAAATCC    540
ATCGACATTT CTCTCGAATC CGAGGACAAA CAACTCTCCA CCGTCACCGT ATCGGCAGCA    600
CGACCACTGG TGAAGATGGA GATAGACCGC CTGTCCTATA ATATGAAAGA TGACCCCGCA    660
GCCAAGACGA ACAACCTGCT CGAAATGCTG CGCAACGTTC CTTTGGTAAC GGTGGATGGT    720
CAGGGCAATA TCCAGGTGAA AGGATCTTCC AACTTCAAAA TCCACCTCAA TGGCAGGCCC    780
TCGACCATGG TGAGCAGCAA CCCGAAGGAG GTCTTTCGCT CCATTCCTGC CCATACGATC    840
AAACGGGTGG AGGTCATCAC CGATCCGGGT GTAAAGTACG ATGCGGAAGG CACAAGTGCC    900
ATCCTGGACA TCGTCACGGA AGAAGGTAAG AAGCTGGAAG GATATTCAGG TTCCATCACG    960
GCCAGTGTCA GCAACAATCC CACAGCCAAC GGTAGTATCT TTCTGACGGC AAAGTCCGGC   1020
AAAGTCGGGC TGACTACCAA CTATAACTAC TACGGTGGCA AAAACAAGGG CTCTCGCTAC   1080
TTTACCGAAC GTACTACATC CATGCTCCAA ACGATAGAAG AAGGCAAAGG GCAAGAAACC   1140
TTTGGCGGAC ACTTCGGCAA TGCCCTCCTC TCATTCGAGA TAGATTCGCT CAATCTCTTT   1200
ACGGTGGGCG GCAATGTACG CCTTTGGGAG ATGACCACCG ACCGGAACAG CGTAGAAAAA   1260
AGCTTTGCCG GCAGCAACCT CATGTCCTAC ATAGACAGAA AACTCAAAAC ACAGATGGAT   1320
GCCGGATCAT ACGAGCTCAA TGCCGACTAT CAGCACAGCA CTCGCCTGCC GGGCGAATTG   1380
CTCACCGTTT CCTACCGCTT CACTCACAAT CCTAATAATA GCGAGACCTT CATTGACCAA   1440
TGGAAGCGCG ATCCGCTCAA CACAGCTAAT ACGATCCAGT ACGCCGGCCA GCACTCCAAA   1500
TCCGATGCGG GCATGGACGA ACATACGGCA CAAGTGGACT ATACACGTCC CTTAGGACAA   1560
GCACATTCTT TGGAAGCAGG GCTGAAGTAC ATCTATCGTC ATGCCACGAG CGATCCTCTC   1620
TATGAGATAC GACCATCCGA AGATGCTCCG TGGCAGCCCG GCTCTCTATA TGCACAGAAT   1680
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CCGTCGAACG GAAAGTTCCG CCACGATCAA TACATCGGAG CAGCCTATGC CGGCTACAAC    1740
TATCGTAAGG ATCAGTATTC TTTGCAAACC GGCCTCCGAG TGGAAAGCAG CAGGCTGAAA    1800
GCACTCTTTC CCGAAAACGC AGCAGCAGAT TTCTCCCACA ACTCGTTCGA CTGGGTGCCA    1860
CAGCTCACGC TCGGCTATAC CCCCTCGCCC ATGAAGCAGC TTAAGCTGGC CTATAACTTC    1920
CGAATCCAAC GTCCTGCAAT CGGCCAACTG AATCCCTACC GGCTACAGAC CAACGATNAT    1980
CAAGTACAGT ATGGTAATCC CGACCTAAAG TCGGAGAAGC GTCACCACGT CGGTCTCTCC    2040
TATAATCAAT ACGGAGCCAA GGTCATGCTT ACAGCATCGC TCGACTACGA CTTCTGCAAC    2100
AACGCCATCC AGAATTACAC CTTCTCCGAC CCGGCCAATC CCAATCTGTT CCACCAGACC    2160
TATGGCAATA TCGGACGAGA GCATTCTTTC AGCTTGAATA CCTATGCCAT GTACACGCCG    2220
GCCGTATGGG TCAGGATTAT GCTCAACGGA AATATCGATC GCACATTCCA AAAGAGCGAA    2280
GCACTCGGCA TTGATGTCAA TTCATGGTCC GGCATGGTAT ACTCAGGCCT GATGTTCACC    2340
CTGCCGAAGG ATTGGACTGT GAATCTCTTC GGAGGTTATT ATCATGGGGG AAGAAGCTAC    2400
CAGACGAAGT ATGATGGCAA TGTATTCAAC AATATCGGTA TAGCCAAACA GCTTTTCGAC    2460
AAAAAATTGA GAGTCTCGCT GAGCGCAAAC AACATTCATG CGAAGTATTC GACATGGAAG    2520
AGCCGGACCA TCGGCAATGG ATTTACTATT TATTCGGAAA ATGCCGGTAT ACAACGGAGT    2580
GTTTCCCTCA GCCTCACCTA CAGCTTCGGT AAGATGAATA CACAAGTGCG CAAGGTAGAG    2640
CGTACGATCG TCAACGACGA CCTCAAGCAA ACCTCATCCC AAGGACAGCA GGGTGGCGGA    2700
CAAGGAAATC CTACCGGCAA T                                              2721
```

(2) INFORMATION FOR SEQ ID NO:3

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

```
ATAATCTTCT GTACGATTCA TCACTCTGAG TTGGAAATAA TGAACAGCAT CATGAAATAT     60
CAATTATATA CGGCCGTCAT AATGGCTCTC TCTGTATCAT CCGTTTGCGG TCAAACCCCA    120
CGAAATACAG AAACCAAACG CCCCGACACG CTGCGCAGGG AGCTTACTAT CGTTAATGAC    180
CAGACTGTGG AGATGGAGCA TGCGGATCCG CTTCCGGCTG CATACAAGGC CATCGAACCT    240
CGATTAAAAC CTTTCCGTCC GGAATATAAC AAGCGTACAT TCGGATTTGT CCCTGAAGTT    300
TCCTCTTCAG GCAGGAACAA TCTTCCGAAT ATCCTGCCGA CGGAAGGTCA TATGAAGCAC    360
CGGGGGTACC TGAATATCGG TATCGGCCAT ACGCTAAACC AGCGAATGGA TGCCGGCTAT    420
CGTCTGATAG ATGCAGAGCA GGAGAGACTG AATCTTTTCC TCTCCTATCG TGGGATGAAA    480
TCGGCTTTCA ATACCGGTGA CTTCGACGGC GACAGAAAGG ATAGACGAAT GATGGCAGGA    540
GTGGACTACG AGCAGCGCAG GCCTTCCTTT GTGCTTGCTA CCGGCTTGTA TTATTCGAAC    600
CATTATTTCA ATAACTACGG ACGGGGAGCT ACCACCAATG TGGGCAGCAT CCCTCAGCTA    660
TCGACACCTG TTACTCCTCA GATGGACAAC GGGACCCACA ACGTCCGTGT ATACTTGGGT    720
GCAAAAAATG ATGTGATCGA TGCCAGGATC GACTATCGTT TCTTCCGTTC TATTCCCTAT    780
CTGGGTACCG ATCCGATGAA GGCTCTCACA GAACATACGC CTGAACTGAA CGTGACGATG    840
AGTAATGAGT TGTCCGATGA TATTAAGCTC GGTGTCGAAG TTCGTACGGG AGGATTGTTT    900
TTTGCCAAAA ACAGCGAAAT GATTCAAACG GGCGTTCTGT CCGAAACCGA CCGCAACCTG    960
TATTATGTGG AGGGCGCGCC CACAATCGGA TTTGTCGGAG ACTCGGACAA TATGCAATGG   1020
AACATACAGG CCGGAGTAGG GATTTCTTCC CATTTCGGAG CCAAAGGGAG GTTGTTTTTC   1080
TGGCCTAAAC TGGATGCTTC GCTTAGTATC TTCCCTTCAT GGCGTGTGTA TGCGAAAGCC   1140
TTCGGCGGTG TGATTCGAAA TGGTCTCGCC GATGTTATGC AAGAGGAGAT GCCCTACCTG   1200
ATGCCCAATA CGATTGTACT CCCTTCGCGC AATGCTTTGA CCGCCCAATT AGGGGTGAAG   1260
GGGAATATAG CCGATGTGGT ACGTATGGAG GTTTATGGCG ACTTCTCCAA GCTGACAGGT   1320
GTGCCTTTCT ATACTCCGAC TCTACCCTTA TATAATCCAT CCGACTTGTA TCAGTATAAT   1380
GTGAGTTTCT TGCCGATATA TGCCGACGGC AGCCGCTGGC GCGCAGGTGG TAAGCTGGAA   1440
TACTCTTATC GCGATATGCT CCGCTTTCTG GTAGACGCAT CCTATGGCAA GTGGAATTTG   1500
GATGGAGGAC TTGTCGCCTC CATGCAGCCC GATCTTATAT TGAAGGCAGA AGTAGGTGTT   1560
CATCCCATTG CCCCATTGGA TGTCAGACTC CGGTATACAC AGCTGAACGG ACGGTATCGG   1620
TATTCTTTCG GCTCGGCTGG CTCGGAAGCC TTGGGTATCG GTAATGTACA TCTTCTTAGT   1680
GCGGATGTTT CATACAAGCT GAAAAAGAAC TTGAGCCTTT ATCTCAAAAT CGATAATATG   1740
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CTGGCGGAAA CGACAGAGCT TATCGGTTAT TATCCTATGC AGCCGTTCCA TTGTTTCGCC 1800
GGTTTTAGCT GGACTTTC 1818

(2) INFORMATION FOR SEQ ID NO:4

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1071 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

AACTCCCATG CAACAGTCTC CGTTATATGT TCAATGATGG AAAAATGTAT CTTTGCTCAC 60
TATCCACATA ACCTTGTGTT CATGATTCGC AAGCATTTCG GTATCATTTT GGGATTTCTT 120
TCTCTTGTGT TTTCGGCAGG TGCTCAACAA GAGAAGCAGG TGTTTCATTT TCTGAACCTT 180
CCGGCTACTG CACAGGCTTT GGCTGCCGGA GGCAAAGCTA TCACCATCGT AGACGACAAT 240
CCCGGACTGG CTTTTGAGAA TCCGGCTCTG CTCGGATATG AATCCGGTGG CCGCGCCTTT 300
CTTTCCTATT TATATTATAT GAGTGGTTCG CATATGGGCA ATGCCTGTTA TGCCTCGTCC 360
GTCGGAGAGC GTGGCATGTG GGGTGTTGGC ATGCGTTTCC TGAACTACGG GTCTATGCAA 420
GGATACGATC AGAATGCGAT TGCCACCGGC TCTTTTAGTG CTTCGGATAT AGCTGTACAA 480
GGATTTTACA GCCATGAACT GAGCAACCAC TTCCGCGGTG GAGTCAGCCT AAAAGCATTG 540

TATTCTTCTA TCGAGACGTA TAGTTCCTTT GGCCTTGGTG TGGATGTCGG TATCAGTTAT 600
TACGACGATG ACAAAGGATA TTCCGCTTCC GCTCTGTTCA AGAACGTAGG GGCGCAACTG 660
AAAGGCTATA ATGAAGAACG GGAACCGCTC GATTGGGATT TCCAGCTCGG CTTTTCCCGC 720
AGTTTTATCA ATGCTCCGTT TCGCTTGCAC ATCACGTTGT TCAATCTGAA TCCGCACTAT 780
TTCAAGCGTC TTGTACCACG CGATCTGTCC AAGATGCAAA AGTTCCTCCG ACACTTCTCG 840
ATAGGAGCAG AATTTACTCC TTCCGAGAGG TTTTGGGTCG GGCTGGGATA TACGCCACAG 900
ATTGCACAGG ATTTCGAGGT GGAAGGCGGC AACAAATGGG GAGGTCTTTC GGCCGGCGTC 960
GGTTTCACTT CAGGTGTAGT ACGTGTAGGC GTATCTGCTG CCACCTATCA TCCTGCAGCT 1020
CTTTCGTTCA TGTGTTCGGT AGGTATCCGT TTGGACGATA AGAGCATCTT C 1071

(2) INFORMATION FOR SEQ ID NO:5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 693 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

AAGTTTATGA TGAAAAAAGC ATTTGTTTTC GTACTACTGG TTTGCCTATT CTCCTCGTTC 60
AGCAGTTCCG CCCAAACAAC GACGAACAGT AGCCGGAGTT ATTTTACAGG ACGAATCGAG 120

AAGGTGAGTT TGAACTTAGG GGTCCCCCCC GTAAGCACAG AGGTTTGGGG AATGACCCAT 180

GATGCGAACG GTCTCCCTTT CGAAATACCT ATCTCTTTCA GTCGTTTCAA CAGCCAGGGA 240

GATATAGCTA CCACTTATTA CATAGCGAAT AGCGAGGCAA CTTTGAATGA ATGGTGCGAC 300

TATGCACACC CGGGCGGCAT CGTGAGGGTA GAAGGTCGTT TTTGGAAAAT GACTTACAAC 360

ATACCAACCT ACAATGCAGT CTGCACCCGG ATTACATTCG AAAATCAAGA AATAGAAGGA 420

ACGATCGTCT TGATACCCAA GCCCAAAGTC TCGCTGCCTC ATGTGTCGGA ATCGGTGCCT 480

TGCATCCGAA CCGAAGCCGG GAGGGAATTT ATCCTTTGCG AAGAAGACGA CACCTTTGTG 540

TCTCACGATG GTAACGAAGT AACGATAGGC GGTAAACCTT TCTTGCTCAA TACCAACGTA 600

AAGATTGTGG GGGACGTATC TCAAAAGTAT GCCGTGGGGG TAGGAGAAAT TCGATTCCTG 660

CAGATTTGTG CCCAAACAGT ATCACAACAA AAA 693

(2) INFORMATION FOR SEQ ID NO:6

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1698 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

TACGACGGAG CGAGACTGGT CTATACCCTA TTTCGGAATA GAAACGACAT TCACCCTATG 60

AAAACCATTG TAAGATACAG CCGCCTTCCG GTCGCTCTCT TCTTTTGCCT TTTGGGAGCT 120
GTGCACTTGT CTGTCGAGGC GCAGATGCTC AATACTCCTT TCGAGCTGTC GGATCAGATC 180
GTCCTGTCTC CCACCGAAAG GCAATACAGG GAGATTTGTG TGCAAACGAA AGAAAAAAGG 240
GGGGCCGATC TTTTCCCGTT GAGCGATAAG CTGCGCGATT CGGCCTATGT TCGTTTCGGC 300
TCGGCCTATG GCGATATTGC GGGCGACTAT CTTCCGTACA ACGGCAATAA CTACTCCTCG 360
CTCTCGCTCG AATCGGGTGG TCGCATCAGT GTCCGTAACT ATGGCACATT GCAGGGCAGT 420
GCTTCCTACT CACGTGGCAT GCACAAACGC ATCGGCTGGA ATGCTCTGCG CAACGCCGAA 480
GCCTACTATC CCTATTTGGT GTCCGATTCG ACCGGCGGAG ACTATCATTT CGAAGACTAT 540
CGGCTTGCCG GCTACTATTC TTTTCGCGCC GGCCGCTTGC CCCTCGGTAT AGGCTTCTCA 600
TACAGGGGCG AAGTTGCTTA TCGGCTGACC GATCCGCGTA CGACCAATAC GACCGGTGCA 660
TTGGAGCTTT CTTGTGCTAC CTCTTTGACG CTGCCTCGAG AGAACAGGCT ATCGCTTTCG 720
GCTGCGTATC TCTATCATAG ACAACACCTC ACACAGTACA ACTGGCGTCC CGGGCAGCAG 780
GACAAATTCT TCGTCAGCTA CGGTTTCGGT CAGGTGGATG TCAGCAACAG CCCTATCTGG 840
TTCGGTATCT CCAGAATGAA CTACGTCAAC GGATGGAAGC TTAGCTCCCG TCTGGATACC 900
CGTAGGGGCG ATGCCATCGG TCTCGACTAC AGCGGCTACT TCCTCGATAC CGAaGAGAGG 960
TCGTCCATCA ATCTCTTTGC TTTGCTTTAC AATCGCCTGC GACTCTATGG TAGCTGGCAT 1020
CTGTCGGACT TCGATTTTTC ATTTTCAGCC GACTATGCTC TGCGCCAAGG GATAGAGCGG 1080
ATATACGAAG ACTACAAGCC GGATGATAAT TATCATATCT ACGACCTCCG TATCTTGGCC 1140
ATTCGCCGCT GGTATATGCT CAATGAGTTT TCTGCCCAAG CCCAAGCCTC CTACCGTATT 1200
CGCACGGATA GAGGTTGTGC CCTGAGAGTG AGTGCCGGTA GTGATTTCTA CGGCTATGAT 1260
GAGACGTATC GCAAGCATGG ACATCATACC ATGAGCGGAA TGCTACGTCC TTTTGCCGGT 1320
ATAGCCTATG ACCATGCCGG ATCCAAATTG GATTTTGGAC TTTCGCTTTC GGCTGCTTAT 1380
CGAATGGTGC TGACGCATTC GTATAAGATT CGTACCATCC AGAAAGAGCA GCTCGACTAT 1440
CAGCTGGCCT ATTTGCCCTA TGCCTATCGT AATAGAGAAG GCGTGGAGGT GCGTTCCTCT 1500
CTGTACGTCT CGATTCCGAT GCAGAATACC CACCGCCTGA TGACAGAGCT GCGGTTGTAT 1560
GGCGACCTGA TGAAAAGAAA GGACGGTATA GCCTATGGCA AAACGCCCGG TGTCATCTCA 1620
CATATCCTGT CCGATCCGCA AGCCGAACGA ACGTCCGGCC ATACCATCGG GGCTATCTGC 1680
AATATCTCCT ACCTCTTC 1698

(2) INFORMATION FOR SEQ ID NO:7

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2457 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

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AGGACGAACG TTTTCTTATC TTTGTCCCAT AAAATTGGGA GAAGGGGTGC TTCCTGTAGC      60
AATCGGAATG CGTGGATGGC TGAGAACAAA CCCTCATCAC CTGAACCGGA TAATACCGGC     120
GTAGGAAACT CTCCGTCTGA CTATCTTCAC GGCGAAGCAA TCATTCCCCC TCTCTCTTCT     180
TTGTCCAACT TCAATGATAA GAGATTTATG AAAAAACTTC ACATGATTGC CGCCTTAGCC     240
GTCCTGCCTT TCTGCCTGAC GGCACAAGCA CCCGTCTCCA ACAGCGAGAT AGATAGTCTT     300
AGCAATGTGC AGCTCCAGAC CGTACAGGTC GTAGCTACTC GCGCCACGGC GAAAACCCCT     360
GTCGCTTACA CCAACGTTCG CAAGGCCGAA CTTTCCAAGT CCAATTATGG TCGTGACATC     420
CCCTATCTGC TGATGCTGAC TCCCTCCGTG GTAGCCACCA GCGATGCCGG TACGGGTATC     480
GGATATTCCG GCTTTCGCGT GCGTGGCACC GATGCCAATC GCATCAACAT AACTACCAAT     540
GGAGTACCCC TCAACGACTC CGAATCTCAG TCCGTCTTTT GGGTGAATAT GCCCGACTTC     600
GCCTCTTCCA TCGAAGACCT TCAGGTGCAG CGAGGTGTGG GTACTTCCAC CAATGGTGCC     660
GGAGCTTTTG GGGCAAGTGT CAATATGCGT ACGGATAATT TGGGACTGGC TCCTTATGGC     720
CGTGTCGATT TGAGCGGAGG TTCGTTCGGC ACATTCCGCC GATCGGTCAA ACTCGGTAGC     780
GGACGCATCG GTCGCCATTG GGCAGTGGAT GCCCGCCTGT CCAAAATCGG TTCGGACGGC     840
TACGTGGATA GAGGAAGCGT GGATCTGAAA TCCTATTTCG CACAGGTGGG CTATTTCGGT     900
AGCAACACGG CTCTCAGGTT CATCACTTTC GGAGGAAAAG AAGTTACGGG TATCGCATGG     960
AACGGTCTTT CCAAGGAGGA TGAAGCCAAA TATGGCCGCC GATACAACAG TGCCGGTCTT    1020
ATGTACGTGG ACGCGCAAGG AGTACCGCAC TACTACCACA ATACCGACAA TTACGAGCAG    1080
CGTCACTACC ATGCCATCAT GACGCACAGC TTCTCTCCTT CCGTTATCCT CAACCTCACG    1140
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GCACACTACA CGGCCGGATA TGGCTATACG GACGAATATC GTACCGGACG TAAACTAAAG    1200
GAATATGCAC TGCAGCCCTA TGTGGAAAAC AGTGTGACCG TGAAGAAAAC GGATCTCATC    1260
CGTCAGAAGT ATCTGGACAA TGACTTCGGA GGACTCATCG GTTCGCTTAA CTGGCACACC    1320
GGTGCATGGG ATTTGCAGTT CGGGGCCTCG GGCAATATCT ATAAAGGAGA CCACTTCGGC    1380
CGTATCACTT ACATCAAAAA GTACAATCAG CCCTTAGCTC CCGACTTCGA ATATTATCGG    1440
AACAGGGCAG ACAAAAGAGA AGGTGCAGCC TTTGCCAAAG CCAACTGGCA GATCACTCCG    1500
GAACTGAACA TGTATGCCGA CCTCCAGTAT CGTACCATCG GCTACACGAT AAACGGCATC    1560
ACGGACGAAT ATGATGAGGT ACAGGGAAGT ATGCAGCACA TCGATTTGGA CAAGACCTTC    1620
CGCTTCCTCA ATCCGAAGGC CGGTCTTACC TATAGTTTCG ACGATGCTCA TACTGCCTAT    1680
GCTTCTGTTG CGGTAGCACA CCGCGAGCCT AACAGAACCA ATTACACCGA AGCCGGAATA    1740
GGACAGTATC CTACGCCTGA GCGACTGATC GACTATGAGC TGGGCTACCG CTATGCTTCG    1800
CCCCTCTTGT CGGCCGGAGT AGGTCTCTAT TATATGCAAT ACAAGGACCA ACTCGTGCTG    1860
GATGGCCGTT TGAGCGATGT GGGACAGATG CTCACAAGCA ACGTCCCCGA CAGCTACCGT    1920
ATGGGACTGG AGCTGACTCT CGGTTGGCAG ATCCTTCCTC GTTTGCTGCG TTGGGATGCT    1980
TCTTTCACTA TGAGTCGCAA CAAAATCGAC CGCTACGTAC AATATACATC CGTATATGAT    2040
GCGGACTACA ACTGGCTCGA ACTCAAGGAG GAGACCCTCG AAAGCACGGA TATAGCCTAC    2100
TCGCCCAATG TCATTGCCGG CAGCATGCTT ACCCTCTCTC ATGCCGGTTT CGAAATGGCT    2160
TGGACGAGCC GCTTCGTCAG CAAGCAATAT CTGGACAATA CACAGCGCAG CGATCGCATG    2220
CTTTCCTCCT ATTGGGTGAA CGACCTCCGC CTCGGCTATG TGCTGCCGGT TCACTTCGTT    2280
AAGAGAGTGG CACTGGGCGT ACAGCTCAAT AATCTCTTCA ACCTCATGTA TGCGTCCAAT    2340
GCCTACATCT ACGATGCCGG TTACGTACAG GCATCCGGAG AACTAAGTGC ATATGCCGAT    2400
CTGCGTTATT ATCCTCAGGC CGGATTTAAT GCACTGGGTA NTCTGACAAT CGATTTC       2457
```

(2) INFORMATION FOR SEQ ID NO:8

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 957 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8

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TTTACGTCCG GTACGATATT CGTCCGTATA GCCATATCCG GCCGTGTAGT GTGCCGTGAG    60
GTTGAGGATA ACGGAAGGAG AGAAGCTGTG CGTCATGATG GCATGGTAGT GACGCTGCTC   120
GTAATTGTCG GTATTGTGGT AGTAGTGCGG TACTCCTTGC GCGTCCACGT ACATAAGACC   180
GGCACTGTTG TATCGGCGGC CATATTTGGC TTCATCCTCC TTGGAAAGAC CGTTCCATGC   240
GATACCCGTA ACTTCTTTTC CTCCGAAAGT GATGAACCTG AGAGCCGTGT TGCTACCGAA   300
ATAGCCCACC TGTGCGAAAT AGGATTTCAG ATCCACGCTT CCTCTATCCA CGTAGCCGTC   360
CGAACCGATT TTGGACAGGC GGGCATCCAC TGCCCAATGG CGACCGATGC GTCCGCTACC   420
GAGTTTGACC GATCGGCGGA ATGTGCCGAA CGAACCTCCG CTCAAATCGA CACGGCCATA   480
AGGAGCCAGT CCCAAATTAT CCGTACGCAT ATTGACACTT GCCCCAAAAG CTCCGGCACC   540
ATTGGTGGAA GTACCCACAC CTCGCTGCAC CTGAAGGTCT TCGATGGAAG AGGCGAAGTC   600
GGGCATATTC ACCCAAAAGA CGGACTGAGA TTCGGAGTCG TTGAGGGGTA CTCCATTGGT   660
AGTTATGTTG ATGCGATTGG CATCGGTGCC ACGCACGCGA AAGCCGGAAT ATCCGATACC   720
CGTACCGGCA TCGCTGGTGG CTACCACGGA GGGAGTCAGC ATCAGCAGAT AGGGGATGTC   780
ACGACCATAA TTGGACTTGG AAAGTTCGGC CTTGCGAACG TTGGTGTAAG CGACAGGGGT   840
TTTCGCCGTG GCGCGAGTAG CTACGACCTG TACGGTCTGG AGCTGCACAT TGCTAAGACT   900
ATCTATCTCG CTGTTGGAGA CGGGTGCTTG TGCCGTCAGG CAGAAAGGCA GGACGGC      957
```

(2) INFORMATION FOR SEQ ID NO:9

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION 1...729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

```
TCGACAATAA TGAAAAAAGC TATTCTTTCC GGAGCGGCCT TGCTCCTCGG CCTATGTGCC      60
AACGCACAAA ACGTGCAGTT GCACTACGAT TTCGGTCATT CCATCTACGA CGAACTAGAT     120
GGACGTCCCA AACTGACTAC CACAGTGGAA AACTTCACAC CCGACAAATG GGGAAGCACC     180
TTCTTCTTCA TCGACATGGA TTACACGGGC AAGGGTATCC AGTCGGCCTA TTGGGAGATT     240
TCGCGCGAAC TGAAGTTTTG GCAAGCTCCC GTTTCCATTC ATTTGGAGTA CAACGGAGGC     300
CTCTCCACAA GCTTTACTTT CGGACACGAT GCTCTAATCG GTGCCACCTA CACCTACAAC     360
AACCCCTCCT TTACACGTGG ATTTACGATC ACGCCCATGT ACAAGCATCT GGGTGCGCAC     420
GACTTCCACA CCTATCAGAT CACCGGCACT TGGTACATGC ACTTTCTGGA CGGTCTGCTT     480
ACCTTCAACG GCTTCCTCGA TCTTTGGGGT TTCCCCCAAG AGAACCCAAT CGGGGGCCCT     540
GTGCTCAAAG AAGGGGATAA GTTCGTATTC CTGTCCGAAC CGCAGTTCTG GATCAACCTC     600
AATCGCATCA AAGGCATCGA CAAGGATTTC AATCTCAGCA TAGGGACAGA GATGGAAATC     660
AGCAGGAACT TCGCTCGCAT GGACAAATTC TCCTGCATCC CTACTCTTGC GGTCAAATGG     720
ACTTTCAAC
                                                                     729
```

(2) INFORMATION FOR SEQ ID NO:10

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1350 base pairs
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

```
TGGTGCCAAT CCGACCCAAT ACCTCATTGC CATGCAGTAT ATCGAAACGC TCAAGGACAT     60
CAACAAGGGC GATCAGACCA AGACCGTTTA CCTCCCGTTC GAGGCTACCG GTATGCTCGG    120
TGCCTTGGGC GGTATGAAGG ATTTGGTGAA AGGATGAGAC TCTCTGCCAT TCTTATCGCT    180
TTGATTGTGA TGCTGCCTGC TGTGCTTAGC GGGCAGCATT ATTATTCCAT GGCGGGAGAG    240
CGACTGGAGA CGGACAGCAT TCGTCCGAAC GAACTCTCGG CATCGATCCG AAGTGCGCTT    300
TTCTTTCGGA ACAATGAATA CAATGCACGT TCGGTCAAAG GTTATACGTT GCCGGGTGCA    360
CGGGTTTCCG CTTTTGCCTC TTACTCGCTG CCGGCAGCAC ATGGTGTGAA GCTTTCGCTC    420
GGAGTATCTA CCCTGAACTA CTGGGGGGCA AGTCGCTATC CGGCCGGTAT CGCTTATTCC    480
GATTTACCTT ATTGGACGGA CTATAACGAC TATGTACGCT TGCGTATCCT GCCTTATGTA    540
CAGGCCATGC TGAAGCCGAC GGCCACGACT GCTCTCATGC TGGGCAATAT AGCCGGTGGT    600
ACGGCTCACG GACTGATCGA ACCGATCTAC AATCCTGAGT TGGATTTGAC GGCTGATCCT    660
GAAGCCGGTG TGCAATTTCG GGGTGATTGG ACACGTTTCC GAATGGATGT TTGGGTCAAT    720
TGGATGAGCA TGATTTTCAA AAATGACAAT CATCAGGAGT CGTTTGTCTT TGGCTTGTCC    780
ACTACTTCGA AATTGTTATC GGGTGAAGGC AAATGGCGAC TCGAACTGCC CTTGCAGGCT    840
ATTGCCACGC ATCGCGGCGG GGAATACAAC TGGGCGCAGC AGGATACCGT GCATACATGG    900
GTCAATGGAG CTGTCGGACT TAAGCTTTCG TATCGCCCTC GTACCGACAA ACCCATGCAG    960
ATTTGGGGAT CTGCTTATGG TGTGGCAGCC TTGTCAAGCG GAGGATACTT CCCTTACGAA   1020
AGAGGGTGGG GCGGTTATCT TTCTCTCGGA ATGGACTTGG AGCACTTCGC TTTTCGTACC   1080
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GACTATTGGT ACGGCAGGCA TTACGTTTCT CCCTTTGCTG CACCTTTCGC CAATTCCCTG 1140
ACGTATGACA AACAGCCTCT TACGAACGGT TGGGGCGATT ATATTCGTCT CTATGCCGAC 1200
TATTCGTGGC GGATGGCACG AAGTGTTTCG TTGGCGGCTG TTGCTCGGGT ATGGTTCCAG 1260
CCTTCGGATC GTTTTGCGAT GAGCCACGCC TTGGAACTGA CGATGCGTAT CGATCCCAAA 1320
TTCCCAATAG CTTTTCTGAA AGGCAATCAT 1350

(2) INFORMATION FOR SEQ ID NO:11

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

CCGTTTTCAC CGCCATGGGT ATGTGCTGGA GCGGCTTCCT CAGTACGCAC ACGGCCATGC 60
TCGACAGTCT CAAGTACCGC CGCCTCATCA CACAGGCGAT CGGAGCACAT GCGATCGGCG 120
GACTCGTCGC CGGCATATTC GCCCATTGGC TCTTTGTCCT CATCTCACTC ATTTGATTCG 180
ATACCCGACC AACGTATGAA CAAATCGCTA TTATCATTGG CATGCCTCAT CCTGTGCGGT 240
ATGCCGGCCA TCGCCCAACA GACAGGACCG GCCGAACGCA GCGGCGAGCC TTCTCTGGCC 300
GAACGTGTAT TCGGTCTGGA GCAGAAGCAG AAAAAGCTGA AGGTGTACTT AGGCATACAG 360

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TCGTTCTACG ACCAGCCGCT TGTCGATGAC GAATCCCATA TCGGACACTT CAAGGTACAG    420
GAGCTGCGGA TGTCTGCTCA TGGCGAACTG AACCGCCACC TCAGCTTCGA CTGGCGACAA    480
CGTCTCAACC GTGCCGCCGA CGGCACTTCG TTTGCCGACA ATCTCTCCAA TGCCATCGAC    540
ATCGCAGGTG TGGACTGGCA CCCGAACGAC AAGGTGTCTT TCTTCTTCGG ACGTCAGTAC    600
GCGCGTTTCG GAGGGATAGA ATACGACATG AACCCCGTAG AGATCTACCA GTACAGCGAC    660
CTTGTGGATT ACATGACCTG CTATACTTCG GGCGTGAACT TCGCATGGAA CTTCCACCCC    720
GAACAGCAGC TGCAGCTACA GGTACTCAAT GCTTACAACA ACCGCTTCGC CGACCGCTAC    780
CACGTGACAC CCGATGTCGC TACCGCCACG AGCTACCCGC TCCTCTACTC GGCACAGTGG    840
AACGGTACCC TCCTCGGAGG AGCACTGCAT ATGCGTTACG CCGTGTCGAT GGCTCATCAG    900
GCCCAAGAGC GTAATATGTG GTACTTCACT GCGGGCAACC TGTTCAATCC GGGCAAACGG    960
ATCAACGGAT ACCTCGACCT CACCTACTCG ATCGAGGGAT TGGACGACAA AGGCATTATG   1020
ACTGCTCGCT ACGGCAAGGG CAAGACCCTC ACGGACGTCA AGTACTATGC TCTGGTATCG   1080
AAGTGGAACT TCCGCATTTT CGATCAGGTC AATCTCTTCC TCAAAGGCAT GTACGAGAAC   1140
GGCTATGCGC CTGCCCAATA CGGCGAGAGC AGCCACACGC GCCACTCCTA CGGCTATATG   1200
GGAGGGGTGG AATATTACCC TACGGAGACC AACTTCCGTC TGTTCGTCAC CTACATAGGA   1260
CGGCATTACC GGTACAGTGC GACCGAGACG GAAAGCACCA ATGCTCTTCG CGCCGGTCTG   1320
ATCTATCAGA TACCTTTCTT A                                             1341
```

(2) INFORMATION FOR SEQ ID NO:12

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

```
TACAGGCGAT CGGGAAGGGT TTGTCCTCGT ATCCTCCGGA ACAAACGTTC CTACGCAGAT     60
ACTCGGTTAC AGCCGAGAAG AGCGGTTCGA CTACGAGCCG GCACCAGAAC AAAGATGAAA    120
AGAAGGTTTC TATCGCTGTT ACTGCTGTAC ATACTCTCTT CCATCAGCCT TTCTGCTCAG    180
CGGTTTCCGA TGGTGCAGGG AATCGAGTTG GATACCGATT CGCTTTTCTC TCTGCCCAAG    240
CGTCCTTGGC GCGCCATCGG TAAAACGATA GGCGTCAATC TGGCCGTATG GGGCTTCGAT    300
CATTTCATCA TGAACGAGGA CTTTGCAGAC ATCAGTTGGC AGACTATCAA GAGCAATTTC    360
CAAACAGGCT TTGGCTGGGA CAATGACAAG TTTGTCACCA ACCTCTTCGC ACATCCTTAT    420
CACGGATCGC TCTATTTCAA TGCAGCGAGG TCGAACGGTT TGAGCTTCAG GCACTCTGCT    480
CCGTTTGCCT TCTTTGGCAG TCTCATGTGG GAGCTGCTTA TGGAAAACGA GCCACCGAGT    540
ATCAACGACC TCTGTGCCAC CACCATAGGC GGTATAGCTT TGGGGGAGAT GGGGCACAGG    600
CTGTCGGACC TGCTCATCGA CAATCGTACC ACAGGGTGGG AACGTATGGG GCGCGAGGTG    660
GCTATCGCTC TGATCAATCC GATGCGCTTT CTCAACCGTC TGACAGCAGG AGAGGTGACT    720
TCTGTCGGGA GTCGCAGCGG ACAGATATTT CAGTCTGTCC CCATAAACAT AGTCGTCGAT    780
GCCGGCTTTC GCTTTTTGGC AGACAAGCGG CATGCCCGAA CCGGTGCCAC GGCTCTGACC    840
CTGAATCTGA GATTCGACTA CGGCGATCCA TTCCGAAGCG AGACTTTCTC TCCATACGAT    900
TTCTTCCAAT TCAAAGCCGG ATTGAGTTTC TCCGAATCGC AACCTCTGCT GAGCCAGATC    960
AATCTGATCG GAATCCTAAG CGGATGCCAA CTGCTCGCAC ACGAACGAAC GGTTTTGGTG   1020
GGAGGTCTCT TTCAGCACTT CGACTACTAC AATTCGGAAA AACGAATAAG CAAAAATTCG   1080
GAGGAGGTAC TCGTCACCCC ATACCGTATC TCGCAAGTGG CAGCTCTGGG AGGCGGTCTT   1140
ATCTTCCAGC ACCACGGAAA ATTTCGACGA CGTCCTCTGG AGCTATATGC CGAGACCTAC   1200
CTGAATGTCG TCCCGATGGG AGCCAGTCTG TCGGATCACT ACAACGTGGA CAATCGGGAC   1260
TATAACCTCG GCAGCGGATT GAGCGGCAAG CTATACCTTG GTGCTACGTA CAATGATCTG   1320
TGGAGCTGGC TCTTGGGAGT CGAAAGCTAT CGGCTCTACA CATGGATCGG GTATGAAGAG   1380
CCGCACCAGA AAAATACCGA TGTCAGCTCT TTTATGGTGC AGGGGGACGA AAGCAAGGCG   1440
CGCCTACTGG TGACGAGTTC CGAGTTCGCA TTTCATCCTG GCCCCTGGCA TGTAGCCATC   1500
GTCGCTCGCC GTTTCATCCG CAAAACAGCC TATCAATTCT ACCCTAACGT ATCATTCGAT   1560
ACCGGCGACA TACAGCTGCG TGTCGGATTT CACTTC                             1596
```

(2) INFORMATION FOR SEQ ID NO:13

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 900 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: double
  (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
  (A) NAME/KEY: misc_feature
  (B) LOCATION 1...900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

```
AAAAGAAGAA AAAAACAGAT GAAACGACTG ATTGTTTTTC TGGCAATGGG TGGCTTGCTG     60
TTCACCCTTG CGAACGCACA AGAAGCAAAC ACTGCATCTG ACACTCCCAA AAAGGACTGG    120
ACTATAAAAG GTGTGACCGG ACTAAATGCC TCTCAGACTT CTCTGACCAA CTGGGCTGCC    180
GGTGGAGAAA ACACGGTGGC AGGTAACCTC TATTTGAACA TAGATGCCAA CTACCTGAAA    240
GATAAATGGA GTTGGGACAA CGGTTTGCGT ACAGACTTCG GTCTGACCTA CACAACAGCC    300
AACAAGTGGA ACAAAAGTGT AGACAAGATC GAACTCTTCA CGAAGGCCGG CTATGAGATC    360
GGCAAACATT GGTACGGAAG TGCGCTTTTC ACTTTCCTCT CACAGTATGC CAAAGGATAT    420
GAGAAGCCCT CGGATCACTT GACAGGAGTC AAGCATATCT CTAATTTCTT CGCTCCTGCA    480
TATCTCACTC TCGGTATTGG TGCGGACTAT AAGCCCAATG AGAAGTTCTC TCTCTACCTC    540
TCTCCTACAA CGGGCAAGCT GACTGTAGTA GCAGACGACT ACCTCTCAAG TTTGGGAGCC    600
TTCGGGGTGA AAGTTGGTGA AAAGACAATG TTCGAACTTG GTGCTTTGGT AGTGGGTTCG    660
GCCAATATAA ATCTGATGGA GAATGTCAAT TTGATAACCA AGGCTTCATT CTTCTCGGCT    720
TATACGCACG ACTTTGGCAA CATTGACATC AATTGGGAGG CTATGCTGGC CATGAAGATC    780
AACAAGTTCC TCACGGCTAC GATAGCCACC AATCTTATCT ACGACGATGA TGTGAAGATC    840
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AACGATGGCC CGAAAATCCA GTTCAAAGAA GTTGTGGGCG TGGGTGTTGC GTACACTTTC
900

(2) INFORMATION FOR SEQ ID NO:14

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2919 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2919

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

```
TTTTACACCG GAATTGACTT GCATATAGAA AGCCAAATGA AGAAACTTTT CCCATTATTA      60
TTACTCATAT TGTCGATTTT GGTCGGATGT GGAAAAAAAG AAAAACACTC TGTAACTGAA     120
ATCGCCNGAG AGAAAAAGCG TATTACTGCA TTGCTGTACG AAAAAGAACT CCCCACTGAT     180
TCTGTTAAAC AGCTTTACGA GAACAGCGTA CAGAACAAGA ACCTTGTGGG ACAAATGTTA     240
TTCGCGATCG AGGTCGGCAA ACGGATGCGT AATATGTCCC AATACACAGA TGCGATGCTA     300
TATCACCAAA AAGGGTTGAA CGCTGCATTG AATCTAAGGG ACACCATCGT AGCCGCACAA     360
GCATGGAATC ATCTCGGAAC GGATAGCCGT CGTATCGGTG CTTTGGCAGA AGCTTCGGAT     420
TATCATTACA AGGCTCTTTC CTTGATAGAA TCTTTTAGCG GAAACCAGAA TAGGCCTGCG     480
ATCAAAGCCA GATCGGCGGC CCTGAACGGC ATCGGCAACA TCAATCTTGA GTTAGGATAC     540
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CATGATGAGG CCGAAAAGAA TTTCCTGAAA GCACTGCAAG GTGAGAAAGA ACTCGACAGT    600
CCTCTCGGGC AAGCTATCAA CTATGCGAAC CTCGGACGTA TCTATCGACA ACGCAAAGAA    660
TACGACAAGG CTCGTACCTA CTTCCTCTTG TCTCTGGAGC AGAACAATAT GGCAGAGAAT    720
CTGATGGGTA TCGGACTCTG TAGCATCAAT CTCGGAGAAG TAGACGAAGA AAAAGGGGAT    780
TATCAAAAGG CTTTGCAAGA GTATGCCACG GCATACAAAC TGATGGAACA GTTGTCCGAT    840
CGATGGCACT GGCTGAATTC CTGTATCCCG ATGGCACGTA TCAATCTCAA ACAAGGTAAC    900
GAAAGGCTCT ACCAGCATTT CATTTCTTTG GCCGAAGGGA CTGCGAAAGA AATTAATTCG    960
ACTTCACATC TGATAGAAAT ATACAATCTT CAATACGAGA ATCTCGAGCG TAAAAAAGAA   1020
TACAAACAAG CCCTCGAAGC ATTCTGTCTG AGCAAGACGT TGAGCGACAG CATGTCCATT   1080
GCGCACAAGG TCAGCAGCAT ACAAGAAACG CGATTCAACT ACGAACGAAA CAAGTCCCAA   1140
AAAGAGCTTG AAGAAATACA GCAAGTAAGC AAGGCAAAAC AAGAGAAATC GAAGTTTATC   1200
CTCTTGAGCA CTCTTTTTGC CCTTTTCATC TCGATTCTTT TGATTTCTGT TCTGACATAT   1260
GCATACCGTC AGGGCAAGAA GCATAACAAG CTGATCAAAG AGACGGATAA ACTTCGCTCC   1320
GGCTTTTTCA CCGGTATTAC ACACGAATTT CGTACGCCTA TCACCGTCAT ACAAGGTTTG   1380
AATGAGAAAA TGAGTTCAAG TCCTGATCTC CAAGCATCGG ACAGAACCGA GCTGCACAAG   1440
ATAATAGACA GACAGAGTAG CCATATGCTG AATTTGGTGA ACCAGCTGTT GGATATTTGC   1500
AAGATCAGAA GCGGAGTATC CACGCCCGAA TGGCGCAATG GCGACATCGT CTCCTTCGTA   1560
CAGATTCTCA TCGATTCGTT TGCACCATAC GCACAGGCTC AAGACATAAC CTTGGAGCTA   1620
CAACCCGAGA GCAAACCTAT TGTCGTGGAC TTCGTCCCCT CCTACTTGCA AAAAATCATA   1680
TCCAATCTTT TGTCCAATGC CATCAAGTAT TCTTTAGCCG GAGGGAGAGT GGTCATATCT   1740
CTGGCAAAAA CCAAGAATGA AAAAAATCTG ATCATACGCG TTGCAGACAA TGGCATAGGA   1800
ATAGATAAAA CTGATCAGGC TCATATCTTC GACATCTTCT ATCGAGGACA GTCCGCTACC   1860
GAAAAGCATG GATCAGGCGT CGGACTCTCG TTTACCAATA TACTGGTCGA AAACCTTCGA   1920
GGTACGATCA AAGTGGAAAG CCAGCCGGGG AAAGGAAGTG CCTTCACCAT CAGTATTCCT   1980
ACACAAAACC AGTCCTCTTC GGCAGAGATT CTTCCTTGGC TACCCTCCTC CGATGACATT   2040
GTCATGCCTG TCCACATCGC GCCCGATGAC TCACCGACAT CTCCGATGGT AGCAGCTCTG   2100
AATCATCGCT TCGAGGACGA ACGTCCGACC ATACTGCTCG TCGAGGACAA TAAGGATATC   2160
AACCTGCTCG TCAAACTACT CCTTTGCGAT CGCTACAATG TGCTATCCGC CGCAAACGGA   2220
AAAGAGGGTA TAGCCCTCGC TACCGAGCAT ATTCCCGACA TTATCATTAC GGATATTATG   2280
ATGCCGATAA TGGATGGGAT AGAAATGACA ATCCGGATGA AGCAATCGCC TCTGCTCTGT   2340
CACATTCCCA TTGTCGCTTT GACGGCCAAG AGTACCGAAC AGGACAGATT GGAAGGAATC   2400
AAAAGCGGTG TAGTCTCTTA TCTATGCAAG CCATTCTCTC CGGAGGAGCT TTTGATGCGG   2460
ATCGAGCAGC TTCTGAAAGA CCGTGAGTTG CTCAAGAAGT TCTATATGCA AAAACTCATG   2520
CTGGATCGGA AGCCGGAGGA GGAGCCTCAA CCGATAGATG ACAGCAGTAT GCAGTTTCTC   2580
CTTGCTGCCA AAGATGCAGT GTCCGGTGGA ATCAAACAAA ATCCGGATTT TTCCGCTCAA   2640
GACTTGGCCG AAAAAATGTG CATGAGTCCA TCCCAACTCA ACAGAAAGCT CACGAGTGTC   2700
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GTAGGTTGCT CCACCATCGG CTACATACAG CAGATCAAGA TAAAATTGGC CTGCAAGCTC    2760
CTTGCCGATG AGAGCAAAAA CATCTCCGAC ATTAGCATTG AGGCAGGCTT TTCGGATCCG    2820
GCTTACTTCT CTCGCACCTT CAAACGCTAC ATGAACTGCT CTCCCTCCCA ATATCGGCAA    2880
AAACTCCTTG CCATGCCGGG GAGCGACAAG GAGACAGTT                           2919
```

(2) INFORMATION FOR SEQ ID NO:15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15

```
TATAAGCAAG CTATAATGAA ACATTTGTTT AAGTCGACAT TAGTACTTCT TTGTGCTCTT      60
TCTTTTTCCG GTACCTATAC CTTTGCACAA GAAAATAATA CAGAAAAGTC ACGATTTGAT     120
TTTTCTGTTA GGCTGGGACA GGGATATATT GCAGGTTCAA CTACCAACCT GATGTATGGG     180
TATACATCTG CTAACGATAG ACTTTTGTCT GGTGCAATTT ATCTGGGCTT GACACCAAGT     240
AAGAAAGAAA ATGCAACCGG CGTAGCATTT CGTTTCTTAT CNCCCTCTCC GGGTTATTAT     300
GTCGATATAT CCGGCAAAGA AAATACCTTG AATTATGCGT TTTACGTTGT CGGAGCATAT     360
AATAGAATAG CCATTCCTAT ACGCCCTATC AAAAATTTTA ATTTCATCTT CTCTACAGAA     420
```

GTCGGAATGG CTTGGATGAG TCGTCATGAG CAAATTTACA ATTCTACTTC GCAGACTTGG 480
GATAAGCAGC GCAAGTCGAG GTCGGGACTG GATTTTGGTC TCGGGATGCA TCTGCAATNC 540
CACATTAATA AGACCGTTTA CTTTATGGCA GGAACCGATC TTACGTCTTG CATGTTCGGA 600
AAAAGGATCA ATGACTACCA GCAAAAGGAT CGAACCTTCA TTGCACTTAT CGACAACAGT 660
ATTGGCATAG GATTAAACCT C 681

(2) INFORMATION FOR SEQ ID NO:16

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 705 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ATGAAAACAA TTAGTAAGAA CCATGCGGCA CGGATCTGTG CCGCCATTGC TTTGTTTGCA 60
GTGTGTAACG GCCGGATAGC TGCTCAGGAT TTTCTCTATG AAATAGGAGG AGGTTTTGGT 120
GCTGCTCAGT ATTTTGGCGA TGCAAACAGA GGCTTGTTCG GTTCATCCGG AGTAGGTTTG 180
GAGTTGGTCG GACGTTACAA TTATAATTTT CGCTGGGCTT TCAGTACCAT GTTGGATTGG 240
CGTACATTGA GAGGCGATAC CGATAAGTCC GGGAATGTCT TCCCCGATTT TGCTCAAGCG 300
GATTTTAAGG TCGGCTTGAC TCAGCTCCAC GTTAGAAGCG AATTTAACTT TCTCCCTTAT 360

AGCGATGGCT ATAAGTATCT TGGTACAGCT CGGCTGTCTC CTTATGTAGC GGCCGGGTTG 420
TCTTTGGGTT TTGCTTCGGG TGCTAAAGGT TCGGCTTTTG CTCCCGGGAT TACTGCGGGA 480
ATGGGAGTGA AGTATAAGCT TAAACCGCGG ATCAATGTCG GTATCGAGTA TTCTTTCACG 540
GGGTTACTTA CCGATGCTTT GGATGCGCTG ACGGATAAAA GTGTTTGGCT CGAGGATCCA 600
TATAAGATCA ATGACTCCTG GGTCAAAAAC AAGGATGCTA CAGGGGCCTT AGTGCTTAGG 660
ATTACGTATG ACTTCGGCCT GCGTAAGACT TTTTGTAATA AACAA 705

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

GCTATTTCTC AGATGAAACG AATACTTCCA ATAGTCGCAT TCCTTTCTCT CTTCCTTGCC 60
CTTGCTTTGC CTGCGAAAGC GCAACGAGCT ATGGGGAAGA CGGCCGACCG TTCGCTAATG 120
GCTTCGGGAC ATTGGGTCAA GATACGTGTC GATGCAAGTG GAGTGTATCG CCTTACGGAC 180
GAACAGCTCC GTGCCAATGG CTTCTCCGAT CCGTCCAAGG TAGGTGTGTT CGGTTATGGT 240
GGAGGGGTGC TTCCCGAAGA TCTGAGCCGG ATCACGACAG ACGATTTGCC TCCGGTACCG 300

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GTACTCCGTC AGGGCAATGC GCTGTATTTC TATGCCGTGG GCCCGGTGAC ATGGTTCTAC    360
AATCCGGCCA AAACCACCAT GGAGCATACG GTGAATACAT ACAGTACGCA TGGCTACTAC    420
TTCCTGTCGG ATGCTGCCGG AGCACCTTTG CAGATGTCCC AATATACGGG TGGAGGTGCG    480
TCGGCCGAGG CTTTGATCGA CTACTACGAT GAGCTGATGC TCCATGAACA GGAATTGTAT    540
TCGCCCAAAG AATCGGGACG AGATCTGTAT GGCGAGTCTT TCAGTGCAGT CAATACGCGT    600
ACGGTCAAGT TCCCTTTGAG GGGCAACACC CGCTCGTCTG GCGAACTCGG TACCGTATTC    660
TCATACATAG CCAAGGCCAG ATCGGCCGGT GGCGGCCGTG AGATGTCGCT CTCGGCGAAT    720
GGCATTCTGA TCTTCAGCGA TCCTTTTTCC ATGACATCGA ATGAAGTCTC CAATTCCTAT    780
TTGGCCGGCA AGAAGCGTCG TCTCTATCAC AGTACGCCGA TGAACAGCTT GGTCAATGAG    840
TTGCGCTTGG ACGCGAACTA TAGCATGACA GGAGATGCGG TCAATCTGGA TTTCATAGAG    900
GTGGCTACAC AGAACGACCT CCGGTACGAT GGCGCACCCA TGCATATCAG GCGGTTTTCC    960
AATTTGCCCG TTTTGGGGGG CGAGTCCTGC CGGTTCGTTA TCAGTGAGGT GCCGGAGTCT   1020
CTGGTGGTTT TGCAGGCCAA TTCTTCCCTG ACAGCATCGC TTGTTCCCGT TAAGACTGTC   1080
GGGGATAAGA CCATTGAGTT CGTGGCTCCG CCGAAGGGTC AGGATCGTAG GACTATCAAT   1140
ACGTTTTATG CCGTGGACTT GTCACAGGCT TCTGCTCCGG AGATCCTCGG AGCGGTACCC   1200
AATCAAAACC TGCATGGAGA GGAAATCCCT GATCTGATCA TTGTCTCTAC TCAGGCGCTC   1260
CTCCTTGAGG CTGATCGACT GGCCACCTAT CGTAGAGAGA AAAACGGGCT GAAGGTTTTG   1320
GTCGTGTTGC AGGAACAGGT GTTCAACGAG TTTTCGGGTG GAACTCCCGA TGCTACAGCA   1380
TACCGCCTCT TTGCCAAAAT GTTCTACGAC AGATGGAAGG CAAATGCACC TGTGGGAGAG   1440
ACCTTCCCGA TGCAAATGCT TCTCTTCGGT GATGGGGCTC ATGACAACAG GAAGGTCTCC   1500
GTAGCTTGGC AGAAACCGTA TCTCCAACAA ACGGAGTTCT TGCTGACATT CCAAGCCGTC   1560
AATTCGACGA ACGTAAACAG TTATGTGACG GATGATTACT TCGGCTTGCT GGATGATCAG   1620
CCGGCCTCGG TCAATATCGG TTGGCGCAAT TATAATATGG CTGTAGGGCG ATTCCCCGTA   1680
CGTACTCCGG CCGAAGCTCG CATCGCAGTG GACAAGACCA TCCGATATGA GGAGGATCGA   1740
GAGAGTGGTG CCTGGCGTAT TCGTGCCTGT TTTGCGGCAG ACAACGGGGA CAAGCACGCA   1800
ACCGAGACTT CCCGTTTGAT CGATACCGTC AAGCGTTATG CTCCTGCCAT CATGCCGGTA   1860
CGCGCCTTTC AGGACGTATA TCCGCATGTC ATCGAGAACG GGTTGCACAG CATTCCGGGT   1920
GCAAAGAAAA AGATGCTGGA AACCCTTCAG TCGGGTATTA TCCTGCTTAA TTATGCTGGT   1980
CATGGCGGTC CTGCCGGATG GTCGGACGAG CATTTGCTGA CGCTCAACGA TATACACAAA   2040
TTCAATTATA AGCATATGCC CATTTGGATT ACTGCCACGT GCGACTTTGC CAACTATGAC   2100
AGTCAGACGA CCTCGGCAGG GGAGGAGGTT TTCCTCCATG AGAAGAGTGG CACTCCGATC   2160
ATGTTCTCGA CTACGCGTGT CGTTTACAAT ACGCAGAATG AGAAGATCAA TGGTTTTATG   2220
CTTCGGCGTA TGTTCGAGAA AGCTAAGGAT GGGCGTTATC GTACGATGGG CGAGATTATC   2280
CGATCGGCCA AACAGGGGAT GCTCAGTACT GTTTTCCCCG ATTCGATCAA CCAGTTGAGT   2340
TTCTTTCTGA TGGGTGATCC GTCCGTGCGT ATGAATCTTC CTACCCACAA AGTGCAATTG   2400
ACCGCAATCA ACGGGCAGGA TCCCGAAGGG CAGTATGGAA CTATTATGCT CAAGTCTTTG   2460
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GAACGGGTAG CTCTGAAGGG TAAGGTAACC GATGAAAAGG GGACATTCGA CGAGACATTC    2520
AGTGGCAAGG TTTTCCTGAC CGTCTTCGAT GGCAGAAAGA AAATGACAGC TTTGGAAGAG    2580
GAGGGAAACG ATCTCTCTCT TGTATATTAT GACTATCCTA ACGTGATGTA TGCCGGTATT    2640
GCCGAGGTGA AAGACGGACT CTTCGAAACT TCGTTTATCG TACCCAAGGA TGTGAACTAT    2700
TCCGAGCACG AAGGCCGGAT CAATCTTTAT GCTTATAACG AGAGCACAAA GGCGGAAGCC    2760
ATGGGGGTAG ACTTCTCCAT CAGAGTCCAA CCGGGTATTC CTGATGAGGT AACGGAAGAT    2820
AATACACCGC CTGAAATCAT AAGCTGCTTC CTCAATGACA GTACATTCCG ATCGGGAGAT    2880
GAGGTTAATC CTACTCCTCT GTTTATGGCC GAAGTATTCG ACTTGAATGG AATCAATATC    2940
ACGGGTAGCG GAGTAGGGCA TGATATTACG CTTTGTATCG ATGGCCGTGC CGACCTGACC    3000
TACAACCTCA ATGCATATTT CACAAGTTCG GCTACGGATG CAGGTGTGGG CACTATTCTC    3060
TTCATGATAC CGGCTTTGGC CGAAGGAGAT CATACTGCCC GACTGACGGT TTGGGACATT    3120
TTCAATAATG CCGTCCATCA TGACTTTTCA TTCAGAGTGG TAGATGGCAT TGCTCCGGAT    3180
GTGGCTGATG TGATTCTATT CCCGAATCCG GTACGCGAGA GTGCTACGTT CCGAATCTTC    3240
CACAATCGCC CCGGAAGCGA TTTGAACGTG GCCGTGGAGA TCTATGACTT CACCGGTCGT    3300
CTTGTGAACA GTTTGCCAGT CAAGACCTAT TCGTCTTCCT ACGGAGAACC TATAGAGATC    3360
AAGTGGGATC TGACCTCCAA ATACGGAGTG AAGATCGGAA ACGGATTCTA CCTCTATCGT    3420
TGTGTGGTGA ACTCTCCCGG AGGACAGACG GCCTCCATGG CCAAGAAAAT GATCGTGGTA    3480
GGACAA                                                               3486
```

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

ATATTCATAG ACCCCGATAA GAATACAAAA CAAAACGAAC GAAATATGAT TATCAAGAAA 60
ATGCTGAAAA ATAAATTGGC CCCCTTGGCC ATACTGTTCC TTTTTGCTCC AAAGGCTATG 120
AAGGCTCAGG AGCAACTGAA TGTGGTACAC ACCTCTGTGC CATCGCTGAA TATCAGTCCG 180
GATGCACGTG CGGCCGGTAT GGGGGATATA GGTGTGGCAA CGACGCCGGA TGCGTATTCA 240
CAGTATTGGA ATCCGAGTAA ATATGCTTTC ATGGATACGA AAGCCGGTAT TAGCTTCTCA 300
TATACACCCT GGCTGTCCAA GCTGGTCAAT GATATTGCCC TGATGCAGAT GACCGGTTTC 360
TACAAATTGG GAACAGACGA GAATCAGGCT ATTAGTGCTT CTCTGCGTTA TTTCACATTA 420
GGAAAGTTGG AGACTTTCGA CGAATTGGGC GAATCCATGG GAGAGGCCCA TCCCAATGAA 480
TTTGCTGTCG ATTTGGGCTA TAGCCGCCAG TTGTCGGAGA ACTTCTCCAT GGCTGTTGCA 540
CTGCGTTACA TCCGCTCAGA CCAAAGCACT CACAACACCG GAGAGAATCA GGCCGGAAAT 600
GCCTTTGCGG CGGATATAGC CGGTTATTTG CAGAAGTATG TGCTACTGGG TAATGCGGAG 660
AGCTTGTGGT CGTTGGGTTT CAACGTAAAG AATATCGGAA CGAAGATCTC CTATGACGGA 720
GGTGTCACGA GTTTTTTCAT CCCTACTTCG TTGAATCTCG GGACGGGGCT GTTGTATCCG 780
ATCGATGACT ATAACAGCAT CAATTTCAAC CTTGAACTTA GCAAGCTGCT TGTACCCACT 840
CCTCCTATCA TGGATCAAAA CGATCAGGCC GGGTATGAGG CTGCACTCAA GAAATATCAG 900
GAAACTTCTT CGATCAGCGG TATATTCTCT TCTTTCGGTG ATGCGCCGGG AGGACTCAAG 960
GAAGAATTCC GTGAGATTAC ATGGGGACTT GGGGCTGAAT ATAGCTATGA CGATAAATTT 1020
TTTGTTCGTG CCGGATATTC ATACCTGCAC CCCACCAAAG GCAATTTGCA GTACTTCACG 1080
GCCGGTGCCG GCTTCAAAAT GAACATATTC CGTATCGATG CTTCCTACCT GTTGTCTACG 1140
ATCCAGAGTA ATCCGTTGGA TCAGACTCTG CGGTTTACGC TTGCTTTCGA TATGGATGGA 1200
TTGCGCAATT TGTTCCAC 1218

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 663 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

```
ACGAGAGAGA GTGTGTTACA TTGTAGAACA AAACTCAAAA AAGAACGAAA AATGAAGAAA      60
ATGATTTTGG CAGCTACTAT GCTGCTCGCA ACAATCGGTT TTGCAAATGC TCAGAGTCGT     120
CCTGCTCTTA GACTGGATGC TAACTTTGTC GGTAGTAACT TAATGCAAAA AGTCGCAAAC     180
ACGAGCGTGA ACAATAAGAT GATCGTAGGC TTACGTGTTG GTGCTGCTGC TGAGTTCGCT     240
CTTAGCAATG ATGGATTCTA TCTCGCCCCC GGATTGGCCT ATACGATGAG AGGTGCTAAG     300
ATGGAATCAC TAAGTGAAAC GACAACTCGC TTGCATTATC TGCAAATACC GGTGAATGCC     360
GGTATGAGAT TTAGCTTTGC TGACAACATG GCTATTTCAT TGGAAGCAGG TCCCTATTTC     420
GCATATGGTG TCGCCGGAAC GATTAAGACT AAAGTTGCAG GCGTTACGGC TTCTGTAGAT     480
GCCTTTGGTG ATAACGGATA TAACCGTTTC GACTTGGGCT TGGGCTTGTC TGCTGCCTTG     540
AGCTACGACC GTTATTACGT ACAAATTGGA TATGAGCATG GATTGCTTAA TATGTTGAAG     600
GATGCTCCGG ATAAGACTTC TTTGCGTAAT CATGACTTCT TTGTGGGTCT CGGTGTTCGC     660
TTC                                                                   663
```

(2) INFORMATION FOR SEQ ID NO:20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1401 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

```
AAAGGTACGT GGAATAGAAA AAACCGAAGA GAAGAAATGA AACGGACAAT CCTCCTGACG     60
GCACTGACCG TCCTATCTTC GCTCTCCTTG CTTCGTGCAC AAAATGAATC CGAAGCATCA    120
ACCAATCCGA TGTCAGGCCT CTCCCTGGAA GACTGTATCC GGATAGCCAA GGAGCGCAAC    180
CTGAATCTGC GCAGACAGGA GATCGAACAA GAAAACCGAA TCATTAGTCT CGATGCAGCA    240
CGACACAGTT TCCTGCCCTC GGTCAATGCA GGCATCGGAC ACAACTATAG CTTCGGACGT    300
TCGAAAGACA AAACGGGAGT AACCGTAGAT CGCTCCTCGA TGAATACCAA- TCTCAGCATC    360
GGAGCTTCGG TGGAAGTATT CAGCGGCACA CGTCGTCTGC ACGACCTCAA GCAGCAAAAG    420
TACAACGTGG AGGATGGTAT AGCCCGACTT CAAAAAGCGC GTGAAGACCT CAGCCTGCAA    480
ATCGCGGCTC TCTATATCAA TTTGCTCTTC CGTCAGGAAA TGACTCGTAC GGCAGAAACA    540
CAGTTGGCAC TGATTCGCGA GCAACGCAAT CGCACGGCCG AAATGGTTCG CGTAGGTAAA    600
TGGGCAGAGG GTAAGCTCCT CGACATAAAT GCCCAGATGG CCAAGGACGA ACAACTTCTC    660
GTACAATATC GTTCGGAGGA GGAGCTGGCT CGTCTGGACT TGGGGCAAGC CCTCGAACTG    720
GAGCACCCCG AAAGCATTGC AGTCAAGGCT CCCGACACAG ACGTTCTCGT AGCAGAAAGG    780
TTGGGATCTC TCCTTGCTCC CGAAGAGATC TATCGCACGG CTCTCGGCTT GAAACCGGCA    840
CTGCATTCGA GCGAGCTGCA AATAGCTTCG GCACGCGAAG GTCTGGCCTC GGCTCGTGCG    900
GCATACTTCC CGACGCTCAG CCTCTCTGCC GGATACAGCA ACGGTTACTT CCGCGACCTC    960
GGCAAGGAGT ATGCCGCCAT CAACCCCTCC TTCTCCGAAC AGTGGAAGAA CAACGGCAGC   1020
TACAGTATCG GACTCTCTTT GAATATCCCC ATCTTCTCTG CCATGCAAAC GCAAGATCGC   1080
```

GTTCGGAGCA GTCGCCTGCA AATACGCTCA AGCGAGCTTC GACTCGTCGA AGAGAAAAAA 1140

GCCCTCTATA AAGAGATCAG GCAAGCATAC AGCAATGCCG TGGCAGCCGA TAAGGCCATC 1200

GCAGCAGCCG AAAACAGCAA GGCCGCTACG CTCAAGGCAT ACGAATACGC TCGCGACAGC 1260

TTCGAGGCAG GGCGCTTGTC TGCCTACGAA TATGCCGAGG CAAAAACAAA ATACGCCCTC 1320

AGCCAAGTGG AAGAACTTCG TGCCAAGTAT GACTTCATAT ACAAAGCCAA AGTTTTGGAT 1380

TTCTATCAGG GCAAAGACTT C 1401

(2) INFORMATION FOR SEQ ID NO:21

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1308 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

AATATAATGT ATAAAGACTA TAAGGGTTTG TATGCGTCGC TTCGGTGGTA TGCCCTGATC 60

ATTGGGTTGC TATTTGCAGC AGACGGTATA CAGGCTCAGA ACAACAACTT TACCGAGTCG 120

CCTTACACTC GCTTCGGCCT TGGCCGTCTC GGAGAACGGA CGACTATTAG TGGGCATTCC 180

ATGGGAGGAC TCGGCGTCGG TCTGCGTCAG GGCACATACG TCAATGCCGT CAATCCTGCT 240

TCATACTCGG CTGTGGATTC GATGACGTTT ATCTTCGATT TCGGTGCATC TACCGGAATT 300

ACGTGGTATG CCGAGAACGG GAAAAAGGAC AATAGGAAAA TGGGAAACAT TGAGTATTTC 360
GCCATGCTTT TTCCTATTTC CAAATCCATT GCTATGAGTG CGGGAGTGCT TCCTTACTCC 420
GCATCCGGGT ACCAGTTCGG ATCCGTTGAT CAAGTGGAAG GAGGCAGCGT CCAGTACACC 480
CGTAAATACT TGGGGACAGG CAATCTGAAC GATCTCTATG TCGGTATAGG TGCAACCCCG 540
TTCAAAAACT TCTCAATAGG AGCCAATGCT TCATCCCTTT TTGGGCGATT CACACACAGC 600
AGGCAGGTAA TCTTCTCCAC GGAGGCTCCT TACAATCCCG TACATCTCTC GACGCTGTAC 660
TTGAAGGCTG CCAAGTTCGA CTTCGGTATG CAGTATCACC TTCTTCTCAA ATCAGATCGT 720
TCGCTCGTTA TCGGTGCCGT CTATTCTCCG CGGGTGAAGA TGCATAGCGA GCTGACTCAG 780
ATAAAGAATC AGGTTCAGAA CGGTGTAGTA GTGGAGAGCG AAACCCAAGA ATATATCAAG 840
GGAATGGACT ATTATACCCT GCCTCATACA TTGGGGATAG GTTTTTCTTA TGAAAAGAAA 900
GATAAACTTC TCTTAGGAGC AGACGTCCAA TATAGTAAAT GGAAAGGCGA GAAATTTTAT 960
AAATCCGATT GCAAATTCCA GGACAGAATA CGGGTATCTC TCGGCGGAGA GATCATACCG 1020
GATATAAATG CCGTTGGGAT GTGGCCTAAA GTTCGCTATC GCTTCGGTTT ACATGGTGAA 1080
AATTCTTACC TGAAAGTGCC GACTAAAGGC GGTGTATATC AAGGATACCA TATCGTAGGT 1140
GCTGTATTCG GTATAGGAAT CCCGCTCAAT GACAGACGTT CGTTCGTAAA TGTCTCTCTT 1200
GAATATGACC GATTGATCCC GAAGGAGGGT ATGATCAAAG AAAATGCTCT GAAATTGACC 1260
TTCGGCCTCA CGTTCAACGA GTCATGGTTT AAAAAGCTGA AACTGAAC 1308

(2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2835 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

```
AATACCATTT CGGAGAATGG GAACGATAGC ACCTATTTTT CTTTTCAAAC TTTTCTTATG     60
CGATCGATTT ATCAATTACT GTTGTCAATA CTCCTTGCTT CTCTTGGTTT CGTCGGGCTG    120
GAAGCCCAAC AAGCCGGAGT AGCAGGTAGA GTATTGGACG AAGAAGGCAA CCCCATGATT    180
CAAGCCAACG TACAGCTTGT ACAGAGTACC GGCCAAGTAG CCGTTGCCGC AGGTGCCACT    240
AATGAAAAAG GGTTGTTCAG CCTGAAAACG TCACAGGAGG GTGACTACAT TCTGCGCGTT    300
TCATATGTAG GTTACACTAC CCACGACGAA AAAATATCTC TTAGAAACGG GCAAACCATT    360
ACGCTCAAAG ATATATCCAT GAACGAAGAT GCCCGTCTTC TACAGAGTGT GACGGTGCAG    420
GCTAAAGCGG CAGAGGTCGT GGTACGCAAC GATACGCTCG AATTCAATGC CGGATCCTAT    480
ACCGTAGCAC AGGGAGCTTC TATCGAGGAA CTGATCAAGA AGCTACCCGG AGCAGAGATC    540
GGATCCGATG GGAAGATCAC CATCAACGGC AAGGACATTA GCAAGATCCT TGTCGATGGC    600
AAAGAGTTTT TCTCCAAAGA TCCACAGGTG GCAATAAAGA ATCTTCCGGC CGATATGGTC    660
AATAAAGTAC AGGTACTGAA CAAACTGAGC GAGCTGTCGC GGATGAGCGG TTTCGATGAT    720
GGAGAAGAGG AGACCGTAAT CAACCTGACG GTGAAGCCCG AAAAAAAGAA AGGCCTCTTC    780
GGAACGCTTC AGGCCGGCTA CGGTACCGAC CAACGCTATA TGGCCGGAGG GAACGTCAAT    840
CGGTTCGATG GAAATAAGCA ATGGACATTG ATCGGTAGTG CGAACAATAC GAACAATATG    900
GGCTTTAGCG AGATGGACAG CGAGATGGGA TCCATGACCT TCTTCTCTCC CCAAGGCGGT    960
GGTCGACGCG GCTTCGGCAA TAGTGGAGGT GTTACGTCTT CGTCGATGCT GGGCGGCAAC   1020
TTCAGTGTCG AATTCTCCTC TGCCCTTAAT ACAGGAGGCG ATGCACGCTA CGGATACAAC   1080
GACAAGGCCA TAGAGACGAC CAAACGCGTG GAAAATATCC TCGCCGAAGG GAATACTTAT   1140
ATGGACGAAA ATATATTGGA ACGCTCTTTC TCTCACAATG GTCAGGCGCG ATTTAGGATG   1200
CAATGGAAAC CGTCCGAACG TACCGAAGTG GTATTCGAGC CGGATCTTTC GATATCCAAG   1260
ATCGATGGGT TCTTTAACGA CACATACGAG ACGAAAGATG CCACCGGAAT CTCTATCAAC   1320
AAAGGTTCTA TCCACCAAAC TACACAAGGA AACAACTTCA GACTGAACGG AGAATTGGAT   1380
ATCAGTCACA AGCTCAACGA CGAAGGCCGT ACGATCAGTG CCTCCGTCAG TGGCGGTCTG   1440
ACCGACGAAG ACGGAGATGG CATATATCAG GCTGTGCTCC AAAGCGTGGA GACGAATCAA   1500
AAGCAATTCA ACGACAACTC CAACCTGCAA TATCGGCTTC GCCTCTCGTA TGTGGAACCG   1560
TTGGGTAAAA ACTACTTCGC ACAAGCGATT CTGAACAGAC GTTTCTCCCG TCGCAATTCG   1620
GATCGTGAGG TGTACCGACT GGGCGATGAC GGGCAATACT CCATATTAGA CAGTCAGTAC   1680
GGACTCTCCT ACAGTAACGA GTTCACCCAG TATCGCATCG GACTCAACCT CAAGAAGATT   1740
GCCAAAACGT GGGACTACAC CGTAGGATTC AATGTGGATC CCAACAGAAC TGTCAGCTAT   1800
```

CGGAGCGTAG CCGGAGTAGA GCAGGACAAA CTGGCTTTCA ATCGTGTCAA TCTCTCCCCG 1860

ATGCTCCGAA TCAACTACAA ACCGAGCAGG ACTACCAACC TCCGAGTGGA CTACCGAGGA 1920

CGCACGACAC AACCATCCAT CAATCAGATC GCTCCCGTTC AGGACATCAC GAATCCGCTA 1980

TTCGTGACGG AAGGCAATCC CGGTCTGAAG CCGAGCTATT CCAACAATGT GATGGCCATG 2040

TTCTCGGACT TCGATGCCAA AAGTCAGCGA GCTTTCAACA TTGTTTTCTT CGGCAACTAT 2100

ACATTCGACG ACATCGTCCC CAATACGCAC TACGATCCGT CTACAGGGAT CCGTACCACT 2160

CGTTACGAAA ACGCCTCCGG TACGTGGCAA GCGAATCTTC ATGGGACACT ATCGCTTCCA 2220

CTCAAGAACA GGGCATTTTC TTTCAGGATG TCCTTGTTCA ACAGGTTGGC CGAAGGACAA 2280

AGCTTCATCA ATGACGATAA GAACAAAGCT CTCTCTTTCC GAACGAGGGA ACGCCTGACG 2340

CTGACCTATC GCAACAATTG GATCGATACG AGTATCGGTG GCAATATCGG ATTCTATATG 2400

GCGAATAATA GTCTGAGCGG ACAGAAAGAT TCTCGCACAT ACGATTTTGG CGGCAATTAT 2460

CAAGTTGCCC TAACGCTTCC CTATGGATTC CGTATCGACA GCGATGTTGA ATACAATACG 2520

AACTCCGGTT ACAGCGGAGG ATTCAGTCTG GACGAATGGC TTTGGAATGC TTCGCTTTCA 2580

TACAGCTTCC TCCGTGACAA GGCCGGTACA CTGCGTGTCA ATGGCTATGA CATCCTCGGT 2640

CAGCGGTCAA GTATCAGCCG TTCTGCTTCG GCCATCAATA TAGAAGAGAG CATGTCCAAT 2700

ACGATCGGAC GCTACGTGAT GGTGGACTTT ATCTACCGAT TCAACGCCTT CAGTGGTGGT 2760

GGATCTCGCA GCGATCATCA GCGTGGCAAT ATGAATCGTC CGGGCCCACC TTTCGGCGGT 2820

GGCAGACGAC CGTCC 2835

(2) INFORMATION FOR SEQ ID NO:23

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2370 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

CTCTTGTTTT CTTCTCCTTT ACCCCGAATG GATCGTCCTA AGCCTTCATA TATTGTTCGA 60
ATAGCAGCCA TTCTCTGCTT GTTTGTCGGC AGGCCTTTGT TTGCGCAGAG CTATGTGGAC 120
TACGTCGATC CGCTGATCGG GACGCTAAGT TCTTTTGAGC TGAGTGCGGG CAATACCTAT 180
CCGGTGATCG GTTTACCGTG GGGAATGAAT AGCTGGACAC CGATGACCGG TGTACCCGGT 240
GACGGCTGGC AATATACCTA CTCGGCACAC AAGATTCGCG GATTCAAACA GACCCACCAA 300
CCCAGTCCTT GGATCAACGA CTACGGCCAA TTCTCCCTTC TTCCCCTTAC GGCACCGCAG 360
AAGCCATCAT CGAACGACTC CATAGCTCTG ACTAAATGGT GCAAGCAACT CTTTTCGGAC 420
GAACAGACCT CGTGGTTCTC GCACAAAGCG GAGACGGCGA CGCCATACTA TTATAGTGTC 480
TATTTGGCCG ATTACGACAC ACGCGTGGAG ATGGCTCCGA CCGAGCGTGC AGCTATCTTT 540
CGCATACGTT ATTCCGGCAA TACCGAAAGT GGCTCCGGTC GATGGCTTCG TCTTGATGCC 600
TTTACCGGTG GTTCGGAGAT TAGCATCGTG GATCCTCACA CCGTAGTGGG CATATCTCGC 660
AAGAATAGCG GAGGTGTGCC GGCTAACTTC GCCTGTTATT TCATCCTGCA GTCCGATACT 720
CCTATGGCCG ATGTCCTGCT TGAGACAGAT ACCGGCAAGT CAGACGAAGG CACAAGGGCA 780
TGGGCAGCCT GTCGCTTCGA TTCGCAAGAA GTTACCGTCC GGGTGGCATC TTCTTTTATC 840
AGTGTCGAGC AGGCCGAAAG AAATCTTGCG GAAGTCAAAG GGCAGAGTTT CGACCGGATC 900
AGACTTGCCG GTCGCGAAGC TTGGAATAAG GTGCTCGGAC GCATACATGT GGAAGGAGGA 960
ACGAAGGATG AGCGCACTAC ATTCTATTCC GCACTCTATC GCTGTCTGCT TTTTCCCCGT 1020
CGCTTCTATG AGGAGGATGC TTCCGGCAAT TTTGTGCATT ACAGCCCCTA CAATGGAGAG 1080
GTACTTCCCG GTTATCTCTA TACCGATACC GGATTTTGGG ACACTTTTCG AGCCCTTTTC 1140
CCCCTGCTCA ATCTGCTGTA TCCCGATGAA AACATTAAAA TTCAGGAAGG TCTGCTGAAT 1200
GTATATCGCG AGAGTGGCTT TTTCCCCGAA TGGGCCAGTC CGGGCCATCG GGATTGTATG 1260
ATAGGCAACA ACTCTGCTTC TGTTCTGGCG GATGCCTACC TCAAGGGTGT TCGGGTAGAA 1320
GATACCCGTA CACTGATGAA CGGACTCTTG CATGCTACGA AAGCCGTCCA TCCGAAAATC 1380
TCCTCCACGG GTCGCAAAGG TTGGGAGTGG TACAACTCCT TAGGTTATGT TCCGGCTGAT 1440
GCAGGCATCG ACGAAAGTGC TGCCCGTACG CTCGAATATG CTTATAACGA TTGGTGCATC 1500
CTCCGACTGG GGCGCACATT GGGTTGGGAT AGAGCTGCAT TGGACACGTT GGCTCATCGT 1560
TCGATGAACT ATCGTCATCT GTTCGATCCG GAAACCAAAC TCATGCGCGG TAGAAATCAG 1620
GATGGTAGTT TCCGGACACC TTTTTCCCCT TTCAAATGGG GAGATGTATT CACGGAGGGC 1680
AATGCCTGGC ACTACACTTG GTCGGTCTTT CATGATGTGC AGGGGCTTAT CGACCTGATG 1740

GGAGGAGATC GCCCGTTCGT GTCTATGCTC GATTCGGTAT TCAATACTCC TCCTATGTTC 1800
GATGAGAGCT ATTACGGATT TGTCATCCAC GAAATCAGAG AGATGCAAAT AGCGGATATG 1860
GGCAATTATG CTCATGGCAA TCAACCCATA CAGCATATGA TATATCTGTA TAATCATGCC 1920
GGTCATCCAT GGAAAGCTCA GGAGAGACTA CGCGAAGTGA TGGGGCGGCT CTATCGTCCT 1980
ACTCCGGATG GGTATTGCGG CGATGAAGAC AACGGACAGA CTTCGGCTTG GTACGTTTTC 2040
TCTGCTTTAG GCTTCTATCC TGTTACACCC GCTACGGATC AGTATGTGCT CGGTTCGCCG 2100
ATTTTTTCCA AGGTAATACT CTCTTTTCCC GACGGACACA AAACGGTGTT GCATGCTCCG 2160
GCCAACAGTG CCGATACGCC TTACATCCGC TCGATCAGCG TAGAAGGAAA AGAATGGAGC 2220
TGCAATTACC TGACTCACGA ACAGCTTCGC TCTTCTGCAT CCATTCAATG GATGATGGAC 2280
ACGAAACCCA ATTATAATCG TGGTATGAAG GAAAGTGACA GACCTTATTC CTTCTCCACG 2340
GAGCAACAGC GTCGCGCTAA TCACAGTAAT 2370

(2) INFORMATION FOR SEQ ID NO:24

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

CTAATAATCG AAAAGGAAAT GAAAACAACA GTTCAACAAA TTATTCTGTG CCTGGCTTTA 60

ATGATGTCAG GTGTATTGGG CGGAAACGCA CAGAGCTTTT GGGAAGAAAT AGCTCCTCCT 120

TTTATCAGTA ATGAGCCTAA CGTCAAGTAT ATAATTCCCA ATATGGGGAT TGATTCAAAG 180

GGAACAATCT ATGTAACCGT GACAAAAAGG ATTCAGCAGG GAGCAAATTA TACTTCTGAG 240

CAATTGGGTA TGTACTATCG ACCATTAGGT GATAATGAAC AGTGGTGGAA ACATGATCCG 300

TATTTTGATG ACAAGATAGT TGCGGATATT CAGACAGATG CATATGGCAG AGTTTATGTA 360

TGTACGACTT CTTCTCGAGA TCAAGAGTAT CAACTTTATA TAAACGAGCA GAACGAATGG 420

AGGTGTATAT TCAAAACTTC TGTGTCTACA TATGAGCATG GTATGGCTGT TTTTCGCTCT 480

TCGACAGGGG TGACTTATAT AGGTACCAGG CATCACATCT TCGCATCAGG TGTAAATGAT 540

TTCGAGTTCA ACACTATCTA TGAAGACTCT ACACCTATGA GCTGTCGCTT TGCAGAGGCT 600

ACGAATAGTG GCACCATCTA TCTGGCATTG ATGCATGAAA CCACAATGTC TACGACTATC 660

CTTACTTATC AAAACGGTGA GTTCGTCGAT ATCTCGGAAA GTGAATTGAG TAACTCGATT 720

ATTGCATCCA TGTGCTCTAA TAAAGAAGGT GATATAATAG CTCTTGTTAC TTCATATACA 780

GGATTTATGA GTGGAACCCT TGCGATCAGA AAAGCAGATG AAGGCAAATG GCAACTTGTT 840

GGCGGAGATA TACAGAATGC GATCGTTCAA AATATATGCA TGATGGACGA CAACAAGATT 900

GCTTGTGAAG TCTTCGGGAC TCCTAACGGA GTAGATGGTC GGACAAGGGT TTGTGTTTCT 960

GACGCATCTG TCTTTGATTT TGAGTGGTAT GAAGATGAAA TATACGGAGG CCTGATATTT 1020

GACACTTTCT TCTATAGCCC TTGGGACAAA CTTCTTTATG CGAAATTTGG TGGGATTATG 1080

CTCAGGAGTA AAGAGTCTTT TATAACCTCT TTCATTTCTC CGACAGTTGT ACAAGGAGTG 1140

GATGTCTATA CTTTGGCCGG GAAGATAAGG ATCGAAAGTG AAACTCCGGT GTCTGAGGTG 1200

TTGCTTTTCG ACCTGGCTGG CAGGATGGTA CTTCGGCAAA CCATTGATAA TAAAATCTAT 1260

TCGGACATAG ATACTAACGG ACTAAAGCGA AGCGGTATTT ACGTAGTCTC GGTGCGGCTC 1320

TCTTCCGGAC AGGTATTCAG TCATAAGGTG CAGGTA 1356

(2) INFORMATION FOR SEQ ID NO:25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 993 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

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GGCCTGTACG GTATGTCTGT TGTACCTATA ATAATTTATC TTTGCGGTAT ATCAAATTAT    60
GCAAGACTCA TGATAATCCG GTGTCTTATC CGTCGTCCGA GAACCGTCCT GTTCGGGTTG   120
ATATTCGTGG TAGGTCTTTT CTCTGCGATG GCGCAAGAGA AAAAGGATAG TCTCTCTACG   180
GTTCAGCCAG TGCCGAATAG CAGCATGGTG GAGCAGACCC CTCTTCTCTC CATTGATCAC   240
CCCGTCCTGC CCGCTTCTTT TCAGAATACC CGTACACTGA AAAGGTTTAG AGACAAACAT   300
CTTTCCGATG CTTTGCTCAA TGGATTGAAG CCTCATCGCT CATCTTTGCA ATTGAATGAG   360
GAACTCAACT TCGCGGCAGA GCGTCGGGAT TTCGTTTCTC CCCTCTTGCA AACTCGCCAC   420
GCTGCCGGTG TCCTTTCATG GCGACCGACC GATAGGATGC ATTTTTATAC ATCGGGCAAT   480
ATCGGTCTTG GCCATGATTT ATTGACCGGT GTGCGCAAGG ACTTCGGATG GAATGCTGGT   540
GCCGACTTCT TGCTGAGTCA AAATCTTACG GCACATGTCC AAGGCGGTTG GCAGCAGAAT   600
TTCGGCTTTA TACCTATGAC GGCTGTCAAT GGCCAACTGC GTTGGCAAGC CACCGAGAGA   660
TTGAGTTTTA CCACCGGTAT CGATTATCGA CAGGTACAGT GGAATGCTTT CGATAATAGA   720
ACGTTCTCGC TTAAAGGAAG TGCTCGATAC GAAGTGATGG ACAATGTCTT TGTCAATGGA   780
TTTGGCAGCT ATCCTCTCTA CAGCAGTACG CGCTCAGGAC TCAATATGGC TGTTCCGATG   840
CATGGATTCG GCCCTCAGTA CGGTGGATCG CTTGAGCTGA AAGTCTCCGA GCGATTCGGC   900
TTTGCCGTCG GTATGGAGCG CGAATACAAT ATCTGGACTC GTCGGTGGGA AACGCATTAC   960
TTTGCTTATC CTGTATTCTA TGGCGATAAG AAG                                993
```

(2) INFORMATION FOR SEQ ID NO:26

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26

ATCAAACGAA TAGAAATGAA AAGGATTTTT ACTGTAGCCC TTGTGCTACT TGCTTCGGTC 60

ACTATGGCCA TCGGACAAAG CCGCCCGGCA CTTCGCGTAG ATGCCAACTT CGTAGGCAGC 120

AATCAGAGCA TGAAAAGAGA CGGATATGTG TGGGACACCA AAATGAATGT CGGCCTGCGG 180

GTCGGTGCCG CTGCCGAATT CATGATCGGA TCAAGAGGAT TCTACTTGGC TCCGGGTCTG 240

AACTATACGA TGAAGGGCTC CAAAACCGAA TGGGATATAC CCGAAATGGT TCCTGGTACC 300

TATATTACGA TGGTTTCCAC TCGCTTGCAC TATCTGCAAC TGCCGATCAA TGCCGGCATG 360

CGGTTCGACC TGATGAATGA CATGGCGGTT TCGATCGAAG CGGGTCCTTT CCTTGCATAC 420

GGTATATATG GTACATATCG GCAGAAGTTG GAAGGATGGA AGCCGAACAA CTACAGCACA 480

GAGTTTTTTG GCCCAACGCT TGGTGGCCCA ACAAATATCC GCTGGGACAT CGGGGCAAAC 540

ATAATAGCCG CATTCCACTA TAAGCGTTAT TATATACAGA TAGGCTATGA ACATGGATTT 600

GTGGATATTG TGTCAGGTGG AGGTTCTGAT ATTCCCCGAC TGAACGACAA TAGGCAATCC 660

TCTTCGACGA CCGCTCTAAG AGAAAAGGGA AATAACGAAT ACGCTTATAA TCGTGACTTC 720

TTCGTGGGCA TAGGTTACCG CTTT 744

(2) INFORMATION FOR SEQ ID NO:27

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1689 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

```
TCGCTAATCA ACAATTCAAG AGACTGGAGG GCTCCTGTCC GATTGAGTCT CAAAAAAAAG    60
ACAAAAACTA TGAAGACAAA AGTTTTACGC AAATTCGTGG TGGCGGCTTT CGCCGTCGCA   120
ACCCTCTGTC CTCTCGCCCA AGCGCAGACG ATGGGAGGAG ATGATGTCAA GGTGGTCCAG   180
TACAATCAGG AAAAACTGGT ACAAACGAGG ATGAGTGTGG CGGACAACGG ATGGATCTAT   240
GTAATGACCC ACAGTGGATA CGACACCGGC AATAGCAATG TGAAGATCTT CCGCTCCAAA   300
GACCAAGGTG CCACATACCA AAAGTTGAGG GATTGGGATC CATCGGATGA TTATCAGTTT   360
CAAGACTTCG ATATCGTGGT AACGGGTAAG AATGAATCCG ACATCAAGAT TTGGTCGGTA   420
GAGCTCATGA ATAAGCCCGG AGGATATAAG AGTAGAGTTG CGGTCTTCAG TCGCGATGCC   480
AACGCGCAGA ATGCGAAACT CGTGTATAAG GAAGACTTCT CCAATGTGCA GTTGTACGAT   540
GTGGATATAG CCTCCAACTA TCGTTCGCCT TCTTCTCTTA ACAATGGTGG CAACCCTTTT   600
GCTTTGGCTT TCGCTTACAC CGGCTTCAAC AATACGCACA AAATAAGTTT TGTGGACTAT   660
GTGTTCTCTC TGAATGGAGG GCAAAATTTC AATAAAAACT TACTCTTCAG TCAAGATGGA   720
GAGAAGAAAA TTGACAAGGT GGATCTCTCA TTGGGTAGCA CCTCTGAATC CATGGGTCAC   780
AATGCCTGGC CGCTAATGGG TGTGGTATTC GAAATGAATA AACAAGGGGG AAAAAGCGAT   840
ATCGGTTTCT TGTCGAACTT TGTCGACAAT GATCCCGAAT TTCAGTGGTC AGGCCCTATA   900
AAAGTGAGTG AAAGCGACAT GTCGTTCAGC CCCAAAATCC AAATGTTGCT GGACGAGGAT   960
```

AACAATACGA TCAATGGGGA GAGTTGCCAC AACTTCATGA TTACGTACAG CGATTATGAT 1020
TCTGAATATT CGGATTGGGA CATTCGGTAT GTATATCCCA AGAAATCGTT CAAGTATGAA 1080
AAAGGAAAAA CTCCGACTAT GGATGATCTG GTGGAAGCTT TCCTTACAGC TTCGTACCAG 1140
AGTGAGACCA ACTCGGGGCT GGGGTATGAC AAGAACGCCA ATCACTACCT GATTACATAT 1200
GCCAAAAAAG AAGAGAACGG TACGAACACG CTGAAATACC GCTGGGCCAA TTATGACAAG 1260
ATTCATAACA AAGATTTGTG GAGCGACACA TTTACGTATA CATCATCTGC CAATGCTCTC 1320
TACACACCTC AAGTAGACAT CAATCCGACC AAGGGTCTCG TGTGCTGGTC ATGGGTGGAA 1380
TATCTGCCGG GCAAACGGAT CGTTTGGTCT GATACGCAGT GGACCCATGC CAACGGTGTA 1440
GAAGACATCG TAATGCAAGA AGGCAGCATG AAGCTCTACC CGAATCCGGC TCAAGAATAT 1500
GCTGTGATTA GCCTGCCGAC GGCAGCAAAC TGCAAGGCTG TTGTTTACGA TATGCAGGGC 1560
AGAGTAGTCG CTGAGGCTTC TTTCTCCGGC AACGAATACA GGCTGAACGT GCAGCACTTG 1620
GCTAAGGGTA CGTACATACT CAAGGTCGTA TCCGATACGG AGCGTTTCGT AGAGAAGCTC 1680
ATCGTGGAA 1689

(2) INFORMATION FOR SEQ ID NO:28

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

GGGATAATAT CTGTTCTTTC ACATGTGGTT GACCGTCCAC AATGGGGTGC TTCTCCCGAA 60

GCTGCTGGCA CGCATAGTGT GTATTCGATT CTACATCCCT CCGCCGGTAT TATCCGGATC 120

AGGTCTATGG GTATTATCTC AGCCTGCCGT ATCGCAATTC TTGCCGGCAA GCACCCCCGT 180

AGCGGTCTGT CGAGGGCAAA TGTAGGTATT CTTTCGTACA ATCCAGAAAA CACGCCCGAG 240

AAAAAGAGAA AACTGCAAGA AAAAAATGTT TTCCTCCAAA TCCGGCTCCG TCAATCATTT 300

AATAATTTGA TACCTTCGCT CCCATTTAGA ATCGATAACA CAAAAAAAAT CACTGAAATG 360

AAAAAAACTA CTTTGACAGG ATCGATATGT GCTTTACTCC TGTTTTTGGG TCTCTCGGCC 420

AATGCCCAAT CGAAGTTAAA GATCAAGAGC ATTGAGGCAG CTACCACTTT CAGTTCGGCC 480

ACGGCCGGAA ATGGTTTTGG TGGCAATATC TTCGGCATGG ACATGAGCAT ACGGATGAGG 540

GTACACCACA GCATTCTGCC CGAAGGGTTG GATTTTTCGG TAGGAATACA TGAAAGAAGA 600

GCACACTGGG AAGAGGCCGG AAGTCCGAAG CTCATGTATA CGAATGTCCC AAGTATCATT 660

GGTATTGTTG AAAAGGTAAT AGTCTTCGAA GACGCAGAAG ACTTTTTTGA CAAAAAAGCT 720

CTCGGCCGCT TCCTCATCAG TTTGGGGATA TCCTATACCA AGCATCTGGG AGCGTATTGG 780

GGATGGACCA ATGACGCCCA TATTCTTTTC TCACCGATAC CCAAGAGCAA GGTCCACTAT 840

GACACCTACA CAAGAGCTGG CAGTGACCTT GTACTTCAGT CCGAAGATGT TGCCACAGTG 900

AGCAATGGCT TTTCACCGGG GATCGGACTC AAAAGTTCTA TTTGGTGGAA AATGCCCATC 960

AAGAGCAAAT ATGATTTTCG CCTCGGTTTC AGCCTGGGCT ATGAGTATCT GAACCTGCTA 1020

TATCCGTATC GTAATTTCAA GCTGGATGGA AATAAGCCGC TTTCAGCACT ATCTCCTCGC 1080

ATGAACCACA TCGGCCATGT GGGCTTCAAC TTTACCGTGG GTCTTTGGAC TAAT 1134

(2) INFORMATION FOR SEQ ID NO:29

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...858

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29

```
ATTTGTGGCA GTAAAATGAA TCTATCGGGA TTACAATCTT TCACTATGAT GAAATCCATG     60
CGCAGCGTGC TGTTGCTACT CTTTCCATTG TCTTTGATCA CTGCTTTGGG CTGTAGCAAT    120
AACAAAGCTG CCGAATCGAA GTCTGTCTCT TTCGATTCGG CCTATCTCGA ACGCTACATC    180
CCTCTGCGGG CAGACATAGA TACGCCATCG CTGCATGTGA TGATCAGCTA CGTCTATCCT    240
TCGGGAGATG ATATGCTCAC AGAGATTTTC AACGGTTTGC TCTTCGGCGA CAGCCTGATG    300
GATTCCTCTT CGCCGGAGAA TGCCATGGAA GGCTATGCAC AGATGCTGGG AGAAGACTAT    360
CGCTCTAACA ATGCCGAAGC CAATCTGCAA GGGCTTCCTT CTGACCTTTT GGACTATATC    420
TACAAGCAGG AAAATACCAT CGCTTATTGC GATACGGGAT TGATCTCCAC GCGCATCAAT    480
ACATATACTT ACGAAGGCGG TGCACATACG GAGAATACAG TCCGGTTTGC CAACATCCTT    540
CGCACCACCG GCAAGGTGCT CGAAGAGCGA GATATATTCA AGATCGACTA TGCGGAAAGG    600
CTGTCCGCAC TCATCATAGG ACAATTGGTG CACGATTTCG GCAAGACCAC ACCTGCCGAA    660
TTGGATGCAA TAGGTTTCTT CAACGCAGAA GAAATACAGC CCAATGGCAA TTTTATGATC    720
GATGACAAAG GTCTCACATA CTGTTTCAAT GAGTATCAGA TAGCTGCTTA TGCCAGAGGT    780
GCTGTCTATG TCCGTCTCGG ATATGACGTA TTGGCTCCTT TGCTAAGGGA TGATTCCCCA    840
CTAAAGCGTT ACTTGCCG                                                  858
```

(2) INFORMATION FOR SEQ ID NO:30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1236 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30

```
GGAGAGTATC CTGCAAACAG TAACGACAAA AAAGAGATGG TTATGAAGCT GATTAAAAGA     60
AGTTTGCTCC TGCTTGGAGC GGTACTGCTG ATTACGCTTC CTGCGTACTC GCAGAATGAT    120
GACATCTTCG AAGATGACAT CTATACATCG CGAAAAGAAA TACGTAAACA AAACCAAGTT    180
AAAGACTGGC AAAACCAAGA GGACGGATAC GGCGACGATA CGGAATATAC AGTGGCTTCC    240
GATCGGGACA TTGACGCCTA CAATCGTAGA GATGGCCAGT CCTACGATGG GAAAAAGTTG    300
TCCAAAGACA AGAAAAGAGA CTCCACTCGT TCTTCTGTTC CCGGTCGCTA TAGTCGCCGC    360
TTGGCTCGAT TCTATAAGCC GAATACGATC GTCATTTCAG GTGCCGACAA TGTATATGTA    420
ACTGATGATG GTGAGTATTT CGTCTATGGA GACGAATACT ATGATGACGC GTCGTCTGTA    480
AACATTTACA TCAACAGTCC TTGGTGCGAT CCGTTCCCTT ATACGTCATG GTATCCATCT    540
TTCTCCGGCT GGTACAACTA TACGTGGAAC TATCCATGGT TCTACTACGG TAGCCATATC    600
GGATGGGGCG GTTATTACCC CGGATATAAT TGGTATTGGA GCTACTACTA TGATCCTTTC    660
TACAATCCCT ATGGAATCGG TATGGGTTGG GGATATCCTT ATGGCTGGGG CAGCTATTAC    720
GGTTGGGGTG GCTATCCGGG AGTGATACAT CACTACCACC ACTACCCCAA GAAGACCTAT    780
TCCAATGGTC AGCATTCCGG AGCTTACTAT TCTTATGGCC GACCGAATCG TATCAAAGGT    840
GGAACGTCCG GTGCCAAACT TGGGACAGGA CGCTACGATA GAATTCAAAA TTCGTCTTCG    900
CAAAAAAATA AGTTCGGATT GCAGTCGAAC AAACCCAATA ATAATCTGCA AAATGTCAAG    960
TCGGGACGTA CCGGCCGAGC CAATAGAGAC CGAAATATAG AAACGGTAAC TCCAAACAAC   1020
GGGCAAAAGC AGAATCGTCC CGTATTCCAG CAGAATCAGT CCGGCAATGA CCGACCGACC   1080
GGACGGAATA TCCGCAGCGA GAGACAGGGG GAAAATAACG ATAGGACATT TTCGACTCCT   1140
TCTCGTAGCA ATAGTAACGG TGGCTTCTCC ACGCCTTCTC GCTCTTCTTC CGGCTCTATG   1200
AGCGGAGGTG GCGGACGTAG TGGCCGGGGA CGCAAT                             1236
```

(2) INFORMATION FOR SEQ ID NO:31

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 633 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31

```
AAAAGAAAGA GTATGAAAAG AATGCTGCTG CTTCTCGTTG TATTATTATA TGGAATTGCA    60
GGCCGATTGG CTGCACAAGA CGTTATCAGA CCATGGTCAT TGCAGGTCGG AGCGGGATAC   120
TCCGATACGG AGAACATCCC GGGAGGATTC ACCTATGGTT TCTATTTGGG AAAGCGTATG   180
GGGAGCTTTC TGGAAGTGGG GCTGTCCATG TACAACTCCA CACGTCAAAC AGCCAACAAT   240
GCAGACTCCT TTGCATCGAA CGAAGGAGAC GGATCTTTTC AGGTAAATAT GTCTTCTCCG   300
AATGAGAAGT GGTCATTCTT CGATGCAGGC AGTGCCAACT GCTATATGAT CGTCGTCGGA   360
GTCAATCCTC TCCATCTGTT TTGGCAGAAT AGCCGGCACA ATTTGTTTCT GGCAGTACAA   420
GCCGGCCTGT CCAATAAGCA CAATATTCAT TTCATCTATG GAGACAAGGG AGCCAAAGTC   480
AGTATCTACA CCAATTCGAA TACCTACATC GGTTACGGAG CACGTGTAGC CTACGAATAT   540
CAAATTCATA AAAACGTGGG GGCGGGTGCC GCTGTAATGT ACGACCACGG CAATAAGATG   600
CTTACGGCCA TGGCCACGCT CTCCACTCAT TTT                                633
```

(2) INFORMATION FOR SEQ ID NO:32

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32

```
ATCGTTTACC TTTGTCACTG TATGAACCAC AGACGATCAA AAACCATGCT GACGATCCGA     60
AACTTCCTCC TCTTTTGTTG TCTGTCGCTG ATAGCGTTTG CTGCCGATGC ACAAAGCTCT    120
GTCTCTTCGG GTAGACGACT GACAGAATAT GTCAATCCCT TTATCGGAAC GGCCAATTAC    180
GGTACCACGA ATCCGGGAGC AGTATTGCCC AATGGGTTGA TGAGCGTTAC CCCTTTCAAT    240
GTCAGCGGAT CGACAGAGAA TCGCTTCGAC AAAGATTCGC GTTGGTGGAG TGCGCCTTAT    300
TCGGCCGACA ATAGTTACTG CATCGGTTTC AGCCATGTGA ATCTGAGTGG AGTAGGCTGT    360
CCCGAACTGA GTGGAATACT GCTGATGGCC ACTTCCGGCA CATTCGATCC TGATTACTGC    420
TGCTATGGCT CTTCGCTCAG TCGAGAATAT GCGCGCCCGG GAGAATACAA GGCTGTATTG    480
GACAAATACG GTATAGATGC AGCCGTGACC GTAACCGAGC GGACTGCTTT GACCGAATTT    540
GCTTTTCCCG AAGGAGAAGG CCATATCCTG CTGAACCTGG GACAGGCCCT AAGCAATGAA    600
TCGGGAGCCT CTGTTCGATT CTTAAACGAC TCCACAGTCG TCGGCAGCAG GCTGATGGGG    660
ACGTTCTGCT ACAATCCGCA AGCAGTTTTT CGTCAGTATT TCGTACTTCA GGTGAGTCGG    720
```

CGACCGATCT CTGCCGGCTA TTGGAAGAAG CAGCCTCCTA TGACAGTGGA AGCCCAATGG 780
GATTCGACTG CAGGGAAATA TAAGCAGTAC GACGGCTACA AGCGTGAGAT GAGCGGTGAT 840
GACATCGGTG TCCGATTCTC GTTCAACTGC GATCAGGGGG AAAAGATCTA TGTACGATCG 900
GCCGTTTCAT TCGTCAGCGA AGCCAATGCG CTCTATAATC TGGAAGCGGA GCAAGAAGAG 960
GTGTTCAAAA GTGTCGGAGG GAATCCGGCC AAGGCTTTCT CCGCTATACG CTCTCGCGCT 1020
ATAGAGCGTT GGGAGGAAGC CCTCGGTACG GTGGAAGTGG AAGGAGGCAC ACCGGATGAA 1080
AAGACGATAT TCTATACCGC ACTCTATCAC CTGCTGATAC ATCCGAATAT CCTACAAGAT 1140
GCCAATGGAG AATATCCTAT GATGGGCAGT GGCAAAACGG GTAATACGGC TCACGACCGC 1200
TACACCGTGT TCTCTCTTTG GGACACGTAC CGCAATGTAC ACCCGCTGCT CTGCCTCCTC 1260
TATCCGGAGA AGCAGTTGGA TATGGTACGG ACACTGATCG ACATGTACCG AGAGAGCGGG 1320
TGGCTGCCGA GATGGGAGCT GTACGGACAG GAGACCCTGA CGATGGAGGG CGACCCCTCG 1380
CTTATCGTCA TCAATGACAC TTGGCAAAGG GGCCTTCGTG CTTTCGATAC GGCAACGGCC 1440
TATGAAGCCA TGAAAAAAAA TGCTTCTTCG GCAGGAGCGA CCCATCCGAT CCGTCCTGAC 1500
AACGACGACT ATCTCACCCT CGGCTTCGTA CCGCTTCGCG AACAGTACGA CAATTCCGTA 1560
TCGCATGCGC TGGAATACTA TCTGGCCGAC TGGAATCTGT CCCGGTTTGC CCACGCACTT 1620
GGGCATAAAG AAGACGCAGC TCTATTCGGA AAACGCTCGT TGGGCTACAG ACACTATTAT 1680
AATAAGGAGT ATGGTATGCT GTGTCCATTG CTGCCGGATG GATCATTCCT CACTCCTTTC 1740
GATCCCAAAC AGGGTGAAAA CTTCGAGCCT AATCCCGGTT TCCACGAGGG CAGTGCTTAT 1800
AACTATGCCT TTTTCGTTCC CCACGATATA CAAGGGCTTG CCCGGCTGAT GGGAGGAGCA 1860
AAGGTTTTTT CGGAAAGGTT GCAGAAAGTC TTCGATGAAG GATATTATGA TCCGACCAAC 1920
GAGCCGGACA TCGCCTATCC TTACCTCTTC TCCTATTTCC CCAAGGAAGC ATGGCGAACG 1980
CAGAAATTGA CCCGGGAGTT GATAGACAAA CATTTTTGCA ATGCTCCTAA CGGCTTGCCC 2040
GGTAATGACG ATGCCGGTAC GATGAGTGCT TGGCTTGTCT ATTCCATGCT GGGATTCTAC 2100
CCTGACTGTC CGGGCAGCCC CACCTATACA CTGACCTCGC CGGTATTCCC CCGAGTTAGG 2160
ATTCGGCTCA ATCCGCAGTA TTATCCTCAG GGGGAGTTGA TCATTACGAC CAATACAGAG 2220
AATCAACCGA CAGATTCCAT TTACATCCAT ACGGTTTCTC TTGGCAATAA AACACTTCCG 2280
CATGGAACAA GGCATATCAG CCATGCCGAT TTGGTGCGCT GCGGTCACCT CCGTTACGAA 2340
CTAAGCAATC GTCCTCGA 2358

(2) INFORMATION FOR SEQ ID NO:33

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2859 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2859

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33

```
ATCCGAATGA GAGTATCCGA TCTCTGTTCC AGACTTTCAT GGTTATTACC CGTAATCCTT     60
GTCGGATTGC TCTGTGCTAC TTTGGTCGCT GCGGAACGTC CTATGGCCGG AGCAGTCGGA    120
TTGCACCACC GTCGGCATGC TGCGCTGTCT GATTCTACAG CGAAAGACAC GGTGCCTCTC    180
GCAAAACCTA TTCCTGACAG TGCTTTTCGA GATTCCCTTC CTGCCGATTC CACCGGATCG    240
ATGCGGCAAG ATAGCGTGTA TGACGATGAA TTCGAATTGG AAGATATAGT GGAGTACGAA    300
GCTGCCGATT CCATCGTTTT GCTCGGACAG AATCGTGCCT ATCTTTTCGG CAAGAGCTAT    360
GTGAGCTATC AAAAGAGTCG CTTGGAGGCA AACTTCATGT ATCTCAATAC CGACAGCAGT    420
ACGGTTTATA CTCGCTATGT CCTCGATACG GCCGGTTATC CGATGGCCTT TCCTGTTTTC    480
AAGGATGGAG AGCAGTCGTT CGAAGCCAAG AACTTTACCT ACAACTTCCG CACGGAGAAG    540
GGGATTATCA GCGGAGTGAT CACGCAGCAG GGCGAAGGCT ATCTGACTGC CGGTAAGACC    600
AAGAAGATGC CCGACAATAT CATGTTTATG CAAGGAGGGC GTTATACGAC CTGCGACAAT    660
CACGATCATC CTCACTTCTA TATCAATCTT TCCAAGGCAA AGGTGCATCC GGAGAAAGAC    720
ATCGTCACAG GTCCGGTCAA TCTGGTTATC GCCGATATGC CGCTGCCGAT AGGTCTTCCT    780
TTCGGCTATT TTCCCTTTTC CAACAAATAC TCTTCCGGTA TATTGATGCC CACGTACGGA    840
GAGGACAATC GCTATGGATT TTATTTGAGG AATGGTGGAT ATTATTTTGC CTTCAGCGAC    900
TATATCGATT TGGCATTGCG TGGGGAGATC TTTTCCAAAG GGTCATGGGG CATTTCAGCC    960
CAATCGAAAT ATAAGAAGAG GTATAAGTAC AACGGCTCGT TCGAAGCCAA TTATCTGGTA   1020
TCGAAGTCCG GCGACAAATA CGTGCCCGGA GACTACAGCA AGACCACCAG TCTGAATATC   1080
CGATGGACAC ACAGTCAGGA TCCGAAGGCC AATCCTTTGC AAACGTTGTC GGCCAATGTC   1140
```

```
AATTTTGCCA CCGGGAGCTA TTTCCAGAAT TCGCTGAATA CCACCTATGA TGTCAATGCC    1200
CGTACTGCTA CGACACGAAG TTCGGCCGTG AGCTATTCGC GCAAGTTTCC GGGTACTCCT    1260
TTTTCGATTA CGGGTAGCAT GGATATCAGC CAGAACATGC GCGATACGAC GGTGAGCCTT    1320
ACCTTGCCGA ATCTTTCGAT TAATATGTCC ACGCGTTATC CTTTCAAGCG GAAGACCCGT    1380
GTAGGACCGG AGCGATGGTA CGAGAAGTTG AGTGTGGGCT ATTCCGGTCA GCTTCGCAAT    1440
AGTATCTTGA CAAAAGAGAA AGATTTGCTC CAGAGCAATC TCGTGCGCGA TTGGAAGAAT    1500
GGTATGCGTC ATTCCGTACC GATCAGTTTG ACTGTCCCTT TGTTGGATTA TATCAATCTG    1560
ACTATGGGGG TTAACTACAA TGAGTGGTGG TACACGAAAG GCATACGGAA GTCGTGGAAT    1620
GAGGATAAGA AAACATTCCT GCCTTCGGAC ACGACCTATA AATTCCGCAG ACTGTACGAT    1680
TACAGTCTGT CGGCAGGCTT ATCTACCACA TTGTACGGTA TGTTCAAGCC TTGGAAACCT    1740
TTTTCCTTCG GAGGCAATCT CATTATGATC CGTCATCGCT TCACGCCCAC TGTCAGTTTC    1800
TCCTATATGC CGGACTTCAC GAAACGCCGA TATGGCTTTT GGGAGCTTCT TGAGCATACG    1860
GATCAGAACG GCAAGCTGCA TACGCTGCTC TACTCTCCTT ATTTCGAGCA GATATTCGGT    1920
GCTCCCTCCA TGGGCAATGC AGGATCTGTC AATTTCTCTT TTGACAACAA CTTAGAGGCC    1980
AAGATCAAAT CCAAATCGGA TTCGACAGGG ATCAAGAAGA TCAGCCTGAT AGATCAGTTC    2040
ACATGGTCTA CATCCTATAA TATGTTTGCC GATTCGATCC GATGGAGCAA TATCTCGGCT    2100
TCGCTGGCAC TTCGCCTCTC CAAGAGCTTT ACCTTGCGCT TGTCCGGTCT GTTCGATCCC    2160
TATTTGACGA AGTATTATGA GGGAGAAGAT GGGAAGATCA TTCCCTATAA GAGCAACGAC    2220
CTGCGCATTT TTAACGGCAA GGGATTGGCA CGCCTGATCA GTACGGGTAC TTCTTTCAGC    2280
TATACGCTCA ACAAAGAGTC GCTCAGCGGA TTGATAGCTC TTTTCAGTGG CAAAAAGGAG    2340
CGGAGAGATG AAAAGAAAAA CACAGGGGCT ACTCCTCATG AAGGAGACGA TGCTGCCGAT    2400
ATACTTGAGG GAGGAAGACC GCAAAATGAA AGTGGGGGGT CGCTCCTCGA GCGCAACCGT    2460
CAGGGCGGAG CAGTGGATCA GGATGGTTAC TTCGCATATT CGATCCCATG GAGCCTGTCC    2520
TTCGACTATA GTTGGAATAT TGCTACCGAC TACAATAGGT ACAATGTCAA TAAGATGGAG    2580
CACTACTACC GGGTAACGCA GAATCTGAGC TTTCGCGGCA ATATCCAGCC TACACCGAAC    2640
TGGAGCTTCG GATTCAATGC GAACTACAAT TTCGACTTGA AGAAAATAAC ATCGCTTACC    2700
TGCAACGTCA CTCGCGACAT GCACTGCTGG GCTATCTCGG CCAGTTTCAT CCCTATAGGA    2760
GCATACAAGT CCTATAATTT CGTCATATCG GTGAAGAGTT CACTCTTGCA GGATCTGAAG    2820
TATCAGCAGA GCAATCGTCC CATCACGAAT ACTTGGTAT                           2859
```

(2) INFORMATION FOR SEQ ID NO:34

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1803 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

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AGTAATAGCA GCTCCCACAA GTGGTTAATT TATTATCATA TAGAAAAGAC TAAAAGTATT     60
ATGATCCGCA AGTTGATCTT ACTGCTTGCT CTGATGCCGG TAGCCTCTGT GGCTTTTGCG    120
GTACCAACGG ACAGCACGGA ATCGAAAGAC AATCGTATCC TTACAAGCAT GCAATCCTCC    180
TCTTTGAATA GGGATGATGC TCCGGATAAA TGGCAACCTA TGCATGCCAA TTTCAGTATT    240
CAGAGCGATA TGCTGCTTTC TACTGCCCAA AAGTCCAAGA ACACCTGGTT CGGCAACTCC    300
TATATCATGG GTATAATCAA GAACAATTAT CTGGAGTTTG GTGCCCGTTT CGAGGATCTC    360
TATAAGCCCC TGCCCGGACA TGAACCCGAG ATGNGGCGTG GCGTTCCTCA CATGTATGTG    420
AAGGGAAGCT ATCATTGGGC GGAGCTGACT ATGGGAGACT TCTACGATCA GTTCGGTAGC    480
GGTATGGTAT TCCGCACCTA TGAAGAGCGC AACCTCGGTA TAGACAACGC GGTTCGCGGC    540
GGACGTATAG TACTCACTCC TTTTGATGGA GTGCGTGTCA AGGGTATTGC AGGACAGCAG    600
CGTAACTACT TCGACCGCAC GGGCAAGGTA TTCAATTCCG GCCGAGGCTA CCTACTGGGT    660
TCTGATCTGG AGCTGAATGT AGAGCGTTGG AGCAGTGCCA TGCGCGACAA TGACTATCAT    720
TTGGCTATCG GGGGATCGTT CGTTTCCAAA CACGAAGCAG ACGAAGATAT ATTTGTGGGT    780
GTAGGCGAAG ATCGCAAGCG ACTCAACCTG CCGCTCAATG TCCCGATTAT GGGCCTGCGC    840
ACCAACTTTC AAAAAGGAGG TCTCGCCCTC TACGCAGAGT ATGGATACAA ATACAACGAT    900
CCCTCGGCAG ACAATGACTA TATCTACCAC GACGGACAGG CTGCACTCCT CTCTGCCTCA    960
TACTCCAAAA AAGGGATGAG TATCCTGTTG CAGGCCAAAC GTTGTGAGAA CTTTGCTTTC   1020
CGCAGCAAGC GAAGTGCCCA GCTCACACCG CTTATGATCA ACTATATGCC GGCTTTTACC   1080
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CAAGCTCACA CTTATACGCT GGCGGCCATC TACCCCTATG CTACTCAGCC TCAGGGAGAA    1140
TGGGCTTTCC AAGGTGAACT GCGTTACAAC TTTGCTCGCC GGACAGCTCT CGGTGGACGC    1200
TACGGTACCG GCTTGCGTAT CAACGTTTCG CATGTGCGTG GTCTGGACAA AAAGATGCTC    1260
AAAGAGAATC CCGACGAACT GATCGGAACG GATGGCTACA CCGTTTCTTT CTTCGGCATG    1320
GGCGACCTCT ATTATTCGGA TATAGATGTG GAGATTACTA AAAAGGTAAG CCCAGGATTC    1380
AACTTTACGC TCACCTACTT GAATCAGATC TACAATAACA AGGTACTGCA CGGTGCAGCC    1440
GGAGAGAAGC CTGAGAAGAT CTATGCCAAT ATCTTCGTCT ATGATGGTAA GTATAAGCTG    1500
AGTAATAAGG TAGCCCTCCG TACCGAACTG CAATATTTGC ACACGAAGCA GGATCAGGGT    1560
GACTGGATCT ACGGCATGGC CGAGCTCTCT ATCCTGCCTT CTCTGATGCT TTCCCTCTCG    1620
GAGCAGTATA ATATCGGAGA GACCAAGAAA CATTATGTCA TGGGGTCTGT CACCTATACT    1680
CACGGAGCAC ATCGAGTAGC TTTCTCTGCA GGCAAAACCC GTGCAGGGAT GAACTGCTCG    1740
GGAGGTGTAT GTCGTGTGGT CCCTGAGACT CAGGGATTCT ACCTTTCTTA TAGCACCAAT    1800
CTG                                                                  1803
```

(2) INFORMATION FOR SEQ ID NO:35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2886 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...2886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

```
GCCATTTTTG TCGTATCATT GCAAATTGAA AAAATAACAG AGAATAAGTA TAATTCAGAC     60
AAGAGCATGA ACAAATTTTA CAAATCACTT TTGCAGTCAG GACTGGCTGC CTTCGTGTCG    120
ATGGCAACTG CACTGACCGC TTCTGCACAG ATTTCGTTCG GAGGGGAACC CTTGAGTTTC    180
TCTTCAAGAT CCGCCGGAAC GCATTCATTC GACGATGCAA TGACTATCCG CCTTACTCCG    240
GATTTCAATC CGGAAGACCT GATCGCACAG AGCCGTTGGC AATCGCAAAG AGATGGCCGG    300
CCCGTCCGGA TAGGACAAGT AATACCGGTG GATGTGGACT TTGCATCCAA GGCTTCGCAC    360
ATCTCTTCCA TCGGAGACGT AGATGTATAT CGCCTGCAAT TCAAGTTGGA AGGAGCCAAA    420
GCCATTACGC TTTATTACGA TGCATTCAAT ATTCCGGAGG GCGGACGCCT CTATATCTAT    480
ACCCCCGACC ATGAAATTGT GTTGGGAGCA TATACGAACG CCACTCATCG CCGCAACGGA    540
GCTTTTGCCA CAGAGCCGGT ACCGGGGAGT GAGCTTATTA TGGATTATGA AGTGTCTCGC    600
GGAGGGACTT TGCCTGACAT CAAGATCTCC GGTGCGGGTT ATATATTCGA CAAAGTCGGC    660
GGACGCCCCG TAACGGATAA CCATTACGGG ATCGGTGAGG ACGATTCCGA TTCGGATTGC    720
GAGATCAACA TCAATTGTCC TGAAGGTGCA GACTGGCAGG CAGAGAAGAA CGGTGTGGTG    780
CAAATGATCA TGGTAAAAGG ACAGTATATC TCAATGTGCT CAGGCAACCT GCTCAATAAT    840
ACGAAAGGAG ACTTTACTCC GCTGATCATT TCTGCCGGAC ACTGTGCTTC CATAACAACC    900
AATTTCGGTG TAACGCAATC CGAGTTGGAT AAGTGGATCT TCACTTTCCA CTATGAAAAA    960
AGAGGATGCA GCAATGGTAC ATTGGCCATC TTCCGTGGCA ACAGTATCAT CGGAGCTTCC   1020
ATGAAGGCTT TCCTCCCGAT CAAAGGTAAA TCCGATGGTC TCTTGCTGCA ACTCAACGAT   1080
GAAGTCCCTC TGCGCTATCG TGTCTATTAC AATGGATGGG ACAGTACGCC CGATATTCCC   1140
TCGAGCGGTG CCGGTATTCA TCATCCGGCC GGAGATGCCA TGAAGATTTC CATCCTAAAG   1200
AAGACTCCGG CTCTGAATAC ATGGATCTCC TCCAGTGGTT CCGGAGGGAC TGACGATCAC   1260
TTCTATTTCA AATACGATCA AGGTGGTACG GAAGGAGGAT CGTCCGGTTC TTCTCTCTTC   1320
AATCAGAATA AGCACGTGGT CGGCACACTG ACCGGAGGTG CCGGCAATTG TGGCGGGACG   1380
GAGTTCTACG GCAGACTGAA CAGTCATTGG AACGAGTATG CATCCGATGG CAATACGAGC   1440
CGCATGGACA TCTATCTGGA TCCCCAAAAC AATGGCCAGA CGACCATCCT CAACGGAACG   1500
TATCGTGACG GTTATAAGCC TTTGCCCTCT GTGCCCCGGC TATTGTTGCA GTCTACAGGC   1560
GATCAGGTCG AATTGAATTG GACGGCTGTT CCTGCCGATC AATATCCATC ATCTTATCAG   1620
GTCGAATACC ACATATTCCG AAATGGAAAG GAAATAGCTA CGACAAAGGA GTTGTCCTAT   1680
TCGGATGCCA TCGACGAAAG TATTATCGGT AGCGGTATCA TTCGATACGA AGTAAGCGCA   1740
CGCTTCATTT ATCCCTCGCC GTTGGATGGA GTGGAATCTT ATAAGGATAC GGACAAGACT   1800
TCTGCCGACC TTGCCATAGG AGACATTCAG ACCAAGCTGA AGCCGGACGT AACACCTCTC   1860
CCCGGAGGAG GAGTATCATT AAGCTGGAAA GTTCCTTTCT TAAGCCAGTT GGTTTCCCGA   1920
TTCGGAGAAA GCCCCAATCC TGTGTTCAAA ACCTTTGAAG TGCCCTATGT TTCTGCCGCA   1980
GCCGCACAAA CCCCCAATCC TCCCGTTGGC GTAGTCATTG CAGACAAGTT TATGGCCGGT   2040
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ACATATCCCG AAAAGGCTGC TATCGCTGCC GTTTATGTAA TGCCATCCGC TCCGGACTCT    2100
ACTTTCCACC TCTTCCTCAA GAGCAACACA AACAGAAGAT TGCAGAAGGT GACAACTCCC    2160
TCCGATTGGC AGGCCGGAAC ATGGTTGAGG ATCAATTTGG ATAAGCCGTT CCCGGTGAAT    2220
AATGACCATA TGCTTTTTGC CGGTATCAGA ATGCCTAATA AGTACAAGCT CAATCGTGCT    2280
ATCCGTTATG TAAGAAATCC GGATAACCTT TTCTCCATTA CCGGTAAGAA GATTTCATAT    2340
AACAACGGAG TCTCTTTCGA AGGCTACGGA ATACCCTCGC TCTTGGGCTA TATGGCTATC    2400
AAATATCTGG TGGTAAATAC CGATGCTCCG AAGATCGATA TGTCGCTTGT ACAGGAGCCT    2460
TATGCTAAGG GAACGAATGT GGCTCCATTC CCCGAATTGG TCGGCATATA TGTCTATAAG    2520
AACGGAACAT TTATCGGCAC ACAGGATCCA TCCGTCACAA CTTATTCGGT TTCAGACGGA    2580
ACAGAGAGCG ATGAATACGA AATAAAACTG GTATATAAGG GATCGGGCAT TTCGAATGGC    2640
GTTGCTCAGA TTGAGAATAA CAATGCTGTC GTTGCATATC CGTCTGTTGT AACAGATCGT    2700
TTCAGCATTA AGAACGCTCA TATGGTTCAC GCTGCCGCCC TCTACTCATT GGATGGCAAG    2760
CAGGTTCGTT CTTGGAACAA CCTCCGCAAT GGCGTGACAT TCAGTGTTCA AGGACTTACG    2820
GCCGGTACTT ATATGCTCGT TATGCAGACG GCAAACGGCC CTGTGAGCCA AAAGATCGTG    2880
AAGCAG                                                               2886
```

(2) INFORMATION FOR SEQ ID NO:36

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3936 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...3936

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

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AAGAGGGTAG ATAGCTATGA ATGCAGACAA AAAGCTTGCA AATGTGCAAT TTGTGTGATA     60
CAAAAATTTA CTAATGTAAA ACTAAATGAT ATGCGAAAAA TTTTGAGCTT TTTGATGATG    120
TGCTCTCTGC ATTTAGGTCT ACAATCTCAG ACTTGGCATG GAGATCCGGA CTCAGTGGCA    180
GCCCTACCTT CTATCGGTAT TCAAGAGTCA AGTTGTACCC GAATCACGTT CGAGGTTGTT    240
TTCCCCGGAT TTTATAGTGT GGAAAAACGA GAAGGCAACC AAGTCTTTCA GCGCATTTCC    300
ATGCCGGGTT GTGGCTCGTT TGGGAATCTG GGCGAAGCTG AATTGCCTGT TTTGAAAAAG    360
ATGATAGCCG TTCCGGAATT TTCAACAGCT AACGTTGCTG TAAAAATCAA AGAGACGGAG    420
ACATTCGACA ATTATAATAT CTATCCTAAT CCTACCTATG TCGTAGAGGA GTTGCCTGAG    480
GGGGGACTT ATCTGGTAGA GGCTTTCGCG ATAAACAATG ACTATTATAG CCAAAATGTA    540
AGCCTCCCTT CTACTCACTA TGTCTATTCT CAAGACGGGT ATTTTCGCTC ACAAAGATTT    600
ATCGAAGTTA CCCTGTATCC TTTTCGATAC AACCCTGTCC GACAAGAAAT TCTATTTGCA    660
AAAAAAATCG AGGTTACAAT AACTTTCGAT AATCCTCAGC CACCTTTACA AAAAAACACC    720
GGCATATTTA ACAAAGTAGC CTCCTCTGCA TTTATTAATT ATGAAGCTGA TGGCAAATCG    780
GCGATAGAAA ATGATATGGT GTTCAGTCGT GGTACAACAA CGTACATAAG CGGAAATGTT    840
GCCAGCAACC TCCCTCAGAA CTGTGACTAC TTGGTTATTT ACGATGATAT GTTCAACGTA    900
AATCAACAAC CACACGACGA AATCAAACGG CTGTGCGAAC ATAGAGCCTT CTACAACGGC    960
TTTGATGTAG CTGCTGTAAG TATAAAGGAC GTATTGAATA GCTTCCCATC AAATGCCACC   1020
TCATACATCA ACGAAACTAA ACTGAAAAAT TTCATTCGCT CAGTTTACAA CCAAAGCAAT   1080
GCGAAGAGGA CTTTAGATGG CAAACTGGGA TACGTGCTAC TGATCGGAAA ACCATTGAGC   1140
AAATATTTGG CTGACACTGA TAATACAAAA GTCCCAACCT CTTTTATTCA TAATGTCTCC   1200
TTAATTCCAA GTCATCCAAC TTTTGGTTCC ATATGCGCCT CCGACTATTT TTTTAGTTGT   1260
GTTTCGCCCC TTGATACTGT CGGCGATTTG TTTATCGGTC GATTTAGCGT CACCAATGCT   1320
CATGAATTGC ACAATCTGAT TGAAAAGACT ATCAACAAAG AAATCTCATA TAATCCTATT   1380
GCACACAAAA ATATTCTTTA CGCAGAAGGG AAAGGCTGCG ATGCTCCAAT CTTACGTTTA   1440
TTCTTAAAAG AAATCGCCTC TGGTTACACA GTCAACTCTA TCTTAAAATC TAATCAGGTC   1500
TCTGCAATAG ACTCGATATT TGACTGCTTG AATAATGGTT CCCATCATTT TTATTTTAAC   1560
ACTCATGGAA TGCCGACTGT TTGGGGGATA GGGCAGGGAC TCGACGTCAA TACTCTAACA   1620
GCCCGATTGA ACAATACATC TTCGCAGGGA TTATGTACGA GTCTATCATG TAGTTCGGCT   1680
GTAGCAGATT CAACTATTAG ATCGCTTGGA GAAGTCCTGA CCACATACGC ACCTAACAAG   1740
GGATTCTCGG CTTTCTTAGG AGGAAGCAGA GCCACCCAAT ATGCCGTTTA TTTAGAAGGC   1800
CCCTGTCCTC CGTCAGAATT TTATGAATAT TTACCTTATT CTTTATATCA CAATCTCTCG   1860
ACTGTTGTTG GCGAAATGTT GCTATCATCC ATTATCAATA CTAATTCTGT TGATACGTAT   1920
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TCGAAATTCA ACTTCAATTT GCTTGGCGAC CCTGCACTAA ACATTATGGC TCATGGCATG   1980
GAGGTTAGTA ATTGTATTAC ACTACCAAAC AACACCATTA TAAGCAGTCC GATAACAATA   2040
AAAAATGGTG GCTGCCTAAA AATACCGGAA AAAGGAGTTT TGCATTTTAC TAATAATGGC   2100
TCCATACAAG TCATGTCCGG AGGAACTCTG GAAATAGGCA ATCAGGCTAA AATATCCGGA   2160
GAGACCGGTG CTAACCCCAC CTTTATTACC GTTTACGGCG ATGGTCTTGC GATTAACAAG   2220
CAGGTAGAGA TAGACAATAT AGACCGACTT AACTTGTTTT CTACGCATTC GGTCATGCCC   2280
AAATTTCATT TTGACAGTGT GAAATTCAAC AGTGCCCCGC TGTATACAAC GAACTGTATT   2340
GTGGAGATAA GCAATTGCGA ATTTACCAAT CGAAGTGACA TTATTTCAAA GAATTGTGAC   2400
CTAAGCGTTG AAAACAGTAT GTTTAGCAGT TCGGGGATAA CGGTATTCAA GCCTATGGCT   2460
ACAAGCTCCA TCACCGGATT ATCTACAAAA GCAAAGATTA CCGACAATAC TTTTTTTGCG   2520
ACAGGAAACT TCGCCTACCA TATCACAAAC ACGCCAGGCT TAACAGCAAC CTCCAATGCT   2580
GCCATCAAGT TAGACAATAT TCCTGAGTAT TACATTTCCG GTAATAAAAT AGTCAATTGC   2640
GATGAGGCTC TTGTACTAAA TAATAGTGGC AACAGAACGA ACAGACTCCA CAATATCACA   2700
CGGAATGTGA TAAAAAACTG TAGGATTGGG AGCACGCTTT ATAATTCCTA TGGTATTTAC   2760
AACCGAAATA AGATCAGTAA CAATCATATA GGAGTACGTC TCCTCAACAA CAGTTGTTTT   2820
TATTTCGATA ATGCTCCTGT AATCAATGAA GAAGATAAGC AGACGTTTAT TTCTAATAGG   2880
ACTTGGCAGC TCTATTCATC AAACGGTACA TTCCCTCTCA ACTTCCATTA CAACAGCTTG   2940
CAGGGGGGAG ATACAGATAC ATGGATTTAC AACGACACGT ATACGAATCG CTATATTGAC   3000
GTTTCAAATA ATCACTGGGG CAACAATGAT TTGTTTGATC CGAATCAGGT TTTCAATACG   3060
CCAGACTTGT TCATTTGGAT ACCTTTTTGG GATGGATTGC CAAATGGGAG ATCGGGCAAT   3120
AGCTCTGCTG AAGCAGTAGA ATTCCAAACA GCATTGGACT GTATTGGCAA TAGCGATTAT   3180
CTTTCGGCAA AAGTGGCTCT CAAGATGATG GTTGAAACCT ACCCGGAATC CGACTTTGCA   3240
ATAGCTGCTT TGAAGGAATT GTTCAGGATA GAGAAAATGT CAGGCAACGA TTACGAAGGC   3300
TTGAAAGATT ATTTCAGATC CAATCCAACC ATCATCTCTT CCCAGAACTT GTTCCCGACA   3360
GCTGATTTCC TGTCTGCGCG ATGCGATATT GTGTGTGAAA ACTATCAGTC TGCCATCGAT   3420
TGGTACGAAA ATCGCTTGAA TAGTGAAATC TCCTATCAGG ACAGTGTTTT TGCAGTCATT   3480
GACCTTGGTG ACATTTATTG GAATATGCAG TTAGACTCAC TCAGAGGGAC TGGTATAGAT   3540
TTGAACATAC TTTCCTGTGA ACAAAGGAAA TCGCTCGAAA GCCATCAAAA TGTAAAAAAT   3600
TATTTGTTGT CAACTCTTCC CGAATCAACA GGTACTCTCC TGCCTCCATT AGAATGCAAC   3660
AAATCAAGCC TTGATAAATC CAAGATAATC TCTATTTCGC CCAATCCGGC GAAAGCTGTT   3720
GTAACAATAA TCTACTATAC CGATAACCCT TCCTGTTCTG TAATAAAAAT ATATGGAATA   3780
AATGGAGCCT CGGCTGATAT AACCGGGTTG CCCAAACATC TATCCGAAGG TTATTACAGC   3840
ATACAGTTCA ATACATCCAA CTTTGATCCC GGTTTCTACC TGGTAACGCT AAATGTTGAT   3900
CAGAAAATTA TAGATACGGA AAAATTACGA ATCAAA                             3936
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(2) INFORMATION FOR SEQ ID NO:37

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

TCAGAAAATT ATAGATACGG AAAAATTACG AATCAAATAA TGGCTATCAT GATGAAAAGT 60
ATTGTTTTTA GAGCATTTCT AACGATTTTG CTCTCGTGGG CAGCGATCAC GAATCCGACT 120
GCTCAAGAGA TCTCAGGCAT GAATGCATCC TGTCTGGCTG CTCCGGCTCA ACCGGATACT 180
ATCTTATATG AAAGTTTTGA GAATGGACCT GTTCCCAATG GCTGGCTTGA GATAGATGCT 240
GATGCTGATG GTGCCACTTG GGGAAGCCCA TCAGGCTCTT TCTCTGTACC TTACGGACAC 300
AATGGCCTTT GCACCTACTC CCATATACGT TCCGGTATCT CAACAGCGGG CAACTATCTG 360
ATTACACCCA ATATAGAAGG AGCCAAACGG GTCAAGTACT GGGTATGCAA TCAGTATAGT 420
ACCAATCCGG AACATTACGC AGTAATGGTA TCGACAACGG GGACTGCCAT TGAAGACTTT 480
GTTTTGTTGT TTGATGATTC CATAACAGGG AAACCGACTC CTCTTGTATG GCGTAGACGA 540
ATCGTGGACT TACCGGAAGG GACCAAATAT ATTGCATGGC GACATTACAA AGTCACCGAC 600
TCACACACAG AATTCTTGAA ATTGGATGAT GTCACTGTGT ATAGGTCGAT CGAAGGGCCC 660
GAACCTGCTA CCGACTTCAC AGTAATCAAT ATTGGTCAGA ATGTGGGACG ATTGACTTGG 720
AACTATCCGG AGGATTATCA ACCGGAAGGA AAGGGGAATG AAGAGTTGCA GCTTAGCGGC 780

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TACAACATCT ATGCGAACGG TACACTACTG GCACAAATAA AAGATGTCTC CATACTGGAG    840
TATGTGGACA GCACTTACTC TTTGCGAGAC AATCCCTTGC AAGTGGAGTA CTGCGTTACA    900
GCCGTTTACG ATGAAAGCAT AGAATCTTCG ACCGTATGTG GCACGCTGCA TTACGCCACG    960
GATGCCATCC TTTATGAAAA TTTTGAGAAT GGACCTGTTC CCAATGGTTG GCTTGTGATA   1020
GACGCTGATG GAGATGGATT TAGCTGGGGA CACTATTTGA ATGCATACGA CGCTTTTCCC   1080
GGCCATAATG GAGGCCATTG CTCCTTGTCG GCTTCTTATG TTCCGGGTAT AGGCCCGGTG   1140
ACTCCCGACA ACTATCTGAT TACCCCCAAG GTTGAAGGAG CCAAACGTGT CAAGTACTGG   1200
GTAAGCACGC AGGATGCCAA TTGGGCAGCG GAACATTACG CGGTGATGGC TTCGACAACG   1260
GGGACTGCTG TCGGAGATTT CGTCATATTG TTCGAAGAAA CCATGACAGC GAAGCCGACC   1320
GGCGCATGGT ATGAAAGAAC CATCAACTTA CCTGAAGGGA CTAAATACAT CGCATGGCGG   1380
CATTACAACT GTACCGATAT ATATTTCTTG AAGTTGGACG ATATCACTGT ATTCGGGACT   1440
CCTGCATCAG AGCCCGAACC TGTTACCGAT TTCGTTGTCT CGCTTATTGA AAACAACAAG   1500
GGACGATTAA AGTGGAATTA TCCTAACGGC TACGAACCCG ATAAGACTGA TGATAAAGAC   1560
CCATTGCAGC TTGCCGGCTA CAATATCTAT GCAAACGGCT CGCTCCTTGT TCACATACAA   1620
GACCCGACTG TTTTGGAGTA TATCGATGAG ACTTATTCTT CACGAGACGA TCAGGTGGAA   1680
GTGGAATATT GTGTCACTGC CGTTTATAAC GACAATATCG AGTCCCAATC GGTTTGCGAT   1740
AAGCTGATTT ATGATTCTCA ATCGGACATT ATCTTATATG AAGGCTTTGA GGCCGGAAGT   1800
ATTCCTGAAG GCTGGTTGTT GATTGATGCT GATGGCGACA ATGTTAATTG GGACTATTAT   1860
CCTTGGACTA TGTATGGACA TGACAGTGAG AAGTGTATTG CATCCCCTTC GTACTTACCG   1920
ATGATTGGCG TTTTAACTCC GGATAACTAT TTGGTTACAC CCAGACTCGA AGGAGCCAAG   1980
CTTGTCAAGT ATTGGGTAAG TGCGCAAGAT GCTGTTTATT CGGCTGAGCA TTATGCTGTG   2040
ATGGTTTCTA CTACGGGAAC TGCTGTTGAA GATTTTGTCC TCTTGTTCGA AGAGACAATG   2100
ACCGCTAAGG CTAACGGTGC ATGGTATGAG CGAACTATTA CATTGCCTGC AGGAACAAAA   2160
TATATTGCCT GGCGGCATTA TGATTGCACC GATATGTTTT TCTTGCTCTT GGATGACATT   2220
ACGGTTTATC GTTCTACTGA GACTGTTCCC GAGCCTGTTA CTGATTTCGT TGTCTCGCTT   2280
ATTGAGAATA ACAAGGGTCG CCTGAAATGG AATTATCCTA ACGGCTACGA ACCCGATAAG   2340
ACTGATGATA AAAAACCATT GCAGCTTACC GGCTACAACA TCTATGCAAA TGGCTCGCTC   2400
CTTGTTCACA TACAAGACCC GACTGTTTTG GAGTATATCG ATGAGACTTA TTCTTCACGA   2460
GACGGTCAGG TGGAAATGGA ATATTGTGTC ACTGCCGTTT ATAACGACAA TATCGAGTCC   2520
CAATCGGTTT GCGATAAGCT GAACTATACT ATCACATCCT TGGATAATAT TCAATCTGAT   2580
ACAAGCTTGA AAATATATCC TAATCCGGCA TCGTATGTGG TAAGGATAGA GGGATTGAGT   2640
CGGAGCAAGT CGACAATCGA GTTGTATAAT GCGCTGGGAA TTTGCATATT AAGGGAAGAG   2700
ACTCATTCAG AGAAAACGGA AATCGATGTT TCACGTCTCA ATGACGGAGT CTACTTGATT   2760
AAAGTAGTCG GTGGAAATAA AACAACAACC GAAAAGGTAG AGATAAAGAG GCCG         2814
```

(2) INFORMATION FOR SEQ ID NO:38

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...3753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

AAATGGAAAT TGGCATGCGC TTTTGATTGC GCGTGTTGTT TCGATCCATT TGTAGTAACT 60
AACGAGGTAA TAATAATGAT GAAACGATAT ACAATAATTC TTGCAGTTTT TCTTTTATTC 120
TGCACGGTAT TTACCTTTCA AATAAAAGCT CGCCCTTATG AAAGATTTGC AGATGTAGAG 180
AAGCCTTGGA TTCAGAAACA TTCAATGGAT TCTAAATTGG TGCCTGCAAA TAAGGGTAAC 240
TTAATTCAAG CTGAAATTGT ATACCAATCT GTTTCTGAAC ATAGTGACTT AGTTATTTCA 300
CCTGTGAACG AAATAAGGCC TGCAAATCGT TTCCCTTCGC ATAGGAAGTC TTTTTTTGCA 360
GAAAATCTAC GGGCATCTCC CCCCGTAGTT CCCGTTGCCG TCGACAAGTA TGCGGTACCG 420
GTTGCCAATC CAATGGATCC TGAAAATCCC AATGCCTGGG ATGTGACGCT AAAAATCACT 480
ACTAAAGCGG TAACAGTACC TGTCGATGTG GTGATGGTTA TCGACCAGTC TTCGTCAATG 540
GGAGGGCAAA ACATTGCCAG ATTAAAGTCT GCCATTGCAT CGGGACAGCG TTTTGTGAAA 600
AAAATGTTGC CTAAGGGGAC GGCTACAGAA GGGGTGCGTA TCGCTCTTGT GAGTTATGAC 660
CATGAGCCTC ATCGCTTATC TGATTTTACC AAAGACACTG CTTTTCTCTG TCAAAAAATC 720
CGGGCTTTGA CTCCTATTTG GGGAACACAT ACCCAGGGGG GGCTTAAAAT GGCGAGAAAC 780

ATTATGGCCA CTTCTACTGC TGTGGATAAG CATATCATAT TGATGTCTGA CGGGTTAGCG 840
ACGGAGCAGT ATCCTGTTAA AAATGTAACT ACTGCAGACT TCATTGGCAA AACTGGAAAT 900
GCGAATGATC CCATTGATTT GGTTATACAA GGAGCAATTA ATTTCCCTAC AAATTATGTT 960
TCCAACAATC CATCTACACC TCTTACCCCA AATTATCCAA CTCATTCTTC TAAAGTTGGA 1020
CGGAGAAATC TGCCGGAATC CAAATTCGAT TATAGTAATC TGAGTGCAAG GATTACTTTT 1080
GATGGTGTTG CTGGCGCATT GGTCTATGAA CCGAGGTTTC CTCATCCCTA TTATTATTAT 1140
TTCCCTTGTA ACGCTGCTAT CAATGAGGCT CAGTTTGCGA AAAACTCTGG TTATACAATC 1200
CATACTATTG GCTATGACCT GGGAGATTTT GCCTTGGCCA ACAATTCGTT GAAACTAACC 1260
GCTACAGACG AGAATCACTT CTTTACGGCG ACACCGGCCA ATTTAGCTGC AGCGTTTGAT 1320
AATATTGCCC AAACTATTAA TATAGGTATA CAGAGGGGGG AGGTGACGGA CTTTGTAGCT 1380
CCTGGTTTCA TCGTTAAAAA TCTGACGCAA TCGGGAGATG TTACTCATTT GCTAAATGTT 1440
TCAAATGGAA CGGTGCACTA TGATGTCTCT ACTAAAAAAC TGACATGGAC TACTGGTACT 1500
ATCCTGAGCT CATCAGAAGC TACCATAACT TATCGTATTT ATGCCGATTT GGATTATATA 1560
CAGAACAATG ATATTCCGGT AAATACTACT TCTGCTATCG GCCCGGATCT TGGTGGATTC 1620
GATACCAATA CCGAGGCAAA ATTGACCTAT ACCAATTCCA ATGGCGAACC GAATCAGCAG 1680
TTAATTTTCC CACGTCCGAC GGTTAAGTTA GGTTATGGTG TTATTAAGCG GCACTATGTA 1740
TTGGTAAATA AAGACGGTCA ACCCATACAG GCAAATGGAA CAGTTGTCAG TTCCCTAAGC 1800
GAGGCTCATG TTCTACAGTC ACAAGATTTC TTTTTGCCCT CAGGTGGAGG TCATATTGTT 1860
CCCAAATGGA TAAAGTTGGA CAAAACGACC GAAGCATTAC AGTACTATTC CGTACCGCCG 1920
ACTAACACGG TCATCACTAC TGCCGATGGT AAACGTTATC GTTTTGTCGA AGTCCCAGGC 1980
TCCACGCCGA ATCCGGGCCA AATCGGTATC AGTTGGAAAA AACCGGCAGG AAACGCTTAC 2040
TTCGCTTACA AGCTCCTCAA TTATTGGATG GGAGGAACAA CAGACCAACA GAGTGAATGG 2100
GATGTGACGT CCAATTGGAC AGGAGCCCAA GTACCGCTCA CAGGAGAAGA TGTAGAGTTT 2160
GCAACGACAG AAAATTTCGG TTCTCCGGCG GTAGCCGATT TGCATGTCCG GACAACCAAC 2220
CCCAAAATTA TCGGTAACCT TATCAATAAT TCCGACAAGG ATTTAGTTGT TACCACAAGC 2280
AGTCAATTGA CGATCAACGG CGTGGTTGAG GATAACAATC CGAATGTCGG TACGATCGTC 2340
GTGAAGTCGT CGAAAGACAA TCCTACGGGG ACATTGCTTT TTGCCAATCC GGGCTATAAT 2400
CAAAATGTAG GGGGGACCGT CGAGTTTTAC AATCAGGGAT ATGATTGTGC CGATTGTGGT 2460
ATGTATCGCA GGAGCTGGCA GTATTTCGGT ATCCCTGTCA ATGAATCAGG TTTTCCAATT 2520
AATGATGTGG GCGGAAACGA GACCGTCAAC CAATGGGTTG AGCCTTTCAA TGGCGATAAG 2580
TGGCGGCCAG CACCTTATGC ACCTGATACA GAGCTTCAAA AATTCAAGGG CTACCAGATC 2640
ACGAATGACG TGCAGGCACA GCCTACGGGA GTTTACAGCT TCAAGGGTAT GATTTGTGTG 2700
TGCGATGCCT TCCTGAATCT GACACGCACG TCCGGTGTCA ACTACTCGGG CGCCAACTTG 2760
ATCGGCAACT CATACACTGG AGCCATCGAC ATCAAGCAGG GTATTGTCTT CCCGCCGGAA 2820
GTCGAGCAGA CGGTGTATCT GTTCAACACG GGAACACGCG ACCAGTGGCG TAAGCTTAAT 2880
GGAAGCACGG TTTCAGGCTA TCGAGCCGGT CAGTACCTCT CTGTACCTAA GAATACAGCG 2940

```
GGTCAGGACA ATCTTCCGGA TCGTATTCCA TCGATGCATT CCTTCTTGGT GAAGATGCAG      3000
AACGGAGCGT CTTGTACGTT GCANATCTTG TACGATAAGC TGCTCAAGAA CACGACTGTA      3060
AACAACGGTA ATGGTACGCA GATCACATGG CGATCCGGCA ACTCCGGATC GGCGAATATG      3120
CCGTCACTTG TGATGGATGT TCTTGGTAAC GAGTCGGCCG ACCGTTTGTG GATCTTTACC      3180
GATGGGGGTC TTTCTTTCGG ATTCGACAAC GGCTGGGATG GTCGCAAGCT GACTGAAAAA      3240
GGTTTGTCAC AACTTTATGC GATGTCTGAC ATCGGTAATG ATAAATTCCA GGTTGCAGGG      3300
GTTCCGGAGT TGAATAACCT GCTGATCGGC TTCGATGCGG ATAAGGATGG TCAATACACG      3360
TTGGAGTTTG CTCTTTCGGA TCATTTTGCG AAAGGGGCTG TTTACCTGCA CGATCTTCAG      3420
TCAGGAGCCA AACACCGTAT TACGAATTCT ACGTCGTATT CATTCGATGC CAAGCGGGGA      3480
GATTCCGGGG CTCGTTTCCG CTTGTCATAT GGATGTGATG AGAACGTAGA TGATTCGCAT      3540
GTCGTGAGTA CAAATGGCCG TGAAATTATA ATTCTGAATC AAGATGCTCT TGACTGCACT      3600
GTAACCTTAT TCACAATAGA AGGTAAGCTT CTTCGCCGCT TGAAAGTATT AGCTGGTCAT      3660
AGAGAAGTCA TGAAAGTGCA GACCGGAGGG GCCTATATTG TGCATCTTCA AAATGCTTTC      3720
ACTAATGATG TGCATAAGGT GCTTGTTGAG TAT                                   3753
```

(2) INFORMATION FOR SEQ ID NO:39

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

```
ACTATGGAAG TGAAGAAAAA CACAGTGGTG CTACGCCTTC TGATTTGGTT CGTGGCCATT      60
CTTCTCTTCC ACTCCTCACG GCTGTGGGGA CAGGAAGGGG AGGGGAGTGC CCGATACAGA     120
TTCAAAGGAT TCGTGGATAC CTACCATGCC GTACGCAGCT CTTCTCCTTT TGATTTCATG     180
AGCTCGCGTA CGAGAGTGAG AGGTGAGCTG GAGAGGTCGT TCGGTAATTC GAAAGTAGCC     240
GTATCGGTCA ATGCCACCTA CAATGCTCTA CTGAAAGACG AGACCGGCTT ACGTTTACGT     300
GAAGCCTTCT TCGAGCATCA GGAAGAGCAT TGGGGGTTGC GCCTCGGACG ACAGATTGTC     360
ATTTGGGGGG CTGCCGACGG TGTGCGCATC ACGGATCTGA TCTCCCCGAT GGATATGACC     420
GAGTTTCTGG CACAGGATTA CGATGATATT CGTATGCCGG TCAATGCATT GCGTTTCTCT     480
GTCTTCAACG AATCGATGAA AGTGGAAGTC GTGGTACTGC CTGTATTCGA GGGGTACCGT     540
CTGCCTGTGG ATCCTCGCAA TCCTTGGAAT ATCTTCTCCC TTTCGCCCAT TGCTCAGGGG     600
ATGAATATCG TCTGGAAAGA AGAAGCCGGC AAACCGGCCT TCAAGGTTGC CAATATCGAG     660
TACGGTGCGC GATGGAGCAC TACGCTCTCC GGTATCGACT TCGCTTTGGC TGCATTGCAT     720
ACATGGAACA AGATGCCCGT CATCGAAGTA CAGGGCATTG TGCCGACGGA AATCATCGTT     780
AGCCCTCGCT ATTATCGTAT GGGATTTGTC GGCGGCGACC TCTCCGTACC CGTCGGACAG     840
TTTGTTTTCA GGGGAGAGGC TGCGTTCAAT ATCGACAAAC ACTTCACCTA TAAGAGTCAT     900
GCCGAGCAAG AGGGTTTCCA AACAATCAAT TGGTTGGCCG GAGCCGATTG GTATGCTCCC     960
GGTGAATGGA TGATCTCAGG ACAATTCTCA ATGGAAAGCA TATTCAGGTA TAGGGATTTC    1020
ATCTCCCAAA GACAACATTC TACCCTGATT ACTCTCAATG TTTCCAAGAA ATTCTTCGGC    1080
AGTACACTCC AACTTTCGGA CTTCACCTAC TACGACCTTA CGGGCAAAGG ATGGTTCAGT    1140
CGCTTTGCAG CTGACTATGC CTTGAACGAT CAGATACATC TGATGGCCGG ATATGACTGG    1200
TTCAGTAGTA AGGGCAGCGG TATATTCGAT CGCTACAAAG ACAATTCCGA ACTCTGGTTC    1260
AAAGCCCGCT ACAGCTTC                                                  1278
```

(2) INFORMATION FOR SEQ ID NO:40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 756 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

```
AGGGGGTCGA GTTCGGGCAT TTCAGCCCGT GGACGCGACA TGCGTTCTTT ATTTTTGAGC     60
GCGTTGCGCA GCTCCTCTCT CCATGGTTCA GAGCGACGCA GTCGGATAAG TTCTTCTGTA    120
GTCATGTCAA TAAGGCAGAA AATAAGGTTA TTCCATCTCT CGGTATGCGC CCAAACGCAT    180
GATCATCTCA TCGAAATCCA CTTGGTGTGC ATCGAATTCG GGGCCATCGA CACAGACGAA    240
TTTCGTCTGT CCTCCCACGC TTATACGACA AGCCCCACAC ATACCGGTGC CATCCACCAT    300
AATTGTATTG AGAGAAGCTA TGGTCGGTAT CTCGTAACGT TTGGTCAGGA GAGAAACGAA    360
CTTCATCATC ACAGCCGGCC CGATCGTAAC GCAGAGGTCT ACCGTTTCCC GTTTGATAAC    420
GCTTTCCACT CCATCCGTTA CGAGGCCTTT CGTCCCATAA GACCCATCGT CTGTCATGAT    480
GATCACTTCA TCGCTATTGG CTCGCATTTG TTCTTCAAGG ATAACCAGAT CTTTAGTTCT    540
GGCAGCCAAT ACGACAATTA CACGGTTGCC TGCTTTGTGG AAAGCCTCCA CGATCGGGAG    600
CAAAGGAGCC ACACCCACAC CGCCTCCGGC ACAAACCACT GTGCCGACCT TTTCGATATG    660
CGTACTCTGT CCCAGCGGAC CTACCACATC CGTGATATAG TCGCCGACTT CGAGTTCGGC    720
CAATTTCTTG GAAGATTTGC CCACGGCCTG AACCAC                              756
```

(2) INFORMATION FOR SEQ ID NO:41

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 798 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

```
ATAATTTATA GATCAACAAT GAAACTATTA CTTTATCTCC TATTGGTCTT GTCGACTCTA    60
TCCCCGATGT ATTCGCAAAT GCTCTTCTCA GAGAATCTCA CAATGAATAT AGACAGCACC   120
AAAACCATAC AAGGAACGAT ATTGCCCGTA CTGGATTTCA AAACCGAAAA GGAAAATGTG   180
TTCACCTTCA AAAATACTGC CAATCTCAAT CTGCTGATAA AGCACGGTCA AGTAATCAAC   240
TTAATTAATA AGCTTGAGTT TTCTACCTAT GGCAATAAAG TAACCGTAAG TGGAGGATAT   300
GTACACACCG AATACCGCTA TTTGTTGCAT CATGTTTTTG AGGTTTATCC TTATGTCGAG   360
TCGCAATGGG CAGAAAGTAG AGGAATGAAA TATAAGGTTT CTACGGGATT ACAGTCGCGT   420
TATCGGCTGG TAAATAGTGA TAACTGTCTC ATGTTTGCAA CATTGGGGGT ATTTTTCGAA   480
TTCGAAAAGT GGGAACAGCC AGCCACTAGC CTCTTTGCAG GAACGTATGC ATACAGCCGA   540
AGTATCAAAA GCCACCTGTC TATCAGTTTC AGACATCGGT TGGGTGAACA TTGGGAATTT   600
ACAACTACGG CTATTCACCA GGGAAAGCCT GACAGTTATT TTAAGAAGGC ACGTTTTGGA   660
GGAGCTATCG ACCTCAAATA CCATATCACA CCTACGATAG GAATACGCGG GGCCTATCGG   720
ATCATCTACG ATACTGCCCC TATTGTACCT GTGCGGAAAG ATTACAACAC CGTTGATGTT   780
GGTATCGATA TTTCGTTT                                                 798
```

(2) INFORMATION FOR SEQ ID NO:42

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 987 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

```
GAGACGAACT CTTGGGTATC CAGCGATTGC AATTCGACGA CGATGAAAAC GAATAGACGA    60
TACGCATTTG TTTTGCCGCT TCTGCTACTC ACCGGATTGT TGGCATGGGG GCAGGATTCT   120
TCCCACGGTA GCAATACAGC GTTTGCAACT GATTCTTCGA GTAGAGAGTT GCCCACGGAG   180
CAGTCCGCCT ACCGCATTCA TTCTGCCTAT ATGGTCGGTG GTGGCGGAAG CATAACGCGC   240
GACACCTATT TGTCACCCCT TCGTTATGGA GGATGGACAC TGAATTTGTT GGGAGAGAAG   300
ACGTTCCCTC TCAAAGCCTC CGATTCCCGT TGGATGATCC GTACCGGGCA TGAGCTGGAT   360
TTTGCCCTGA TGGACAATCC GGCCAATAAT GCTCATTTCT ATTCCCTGCT GTATAACGGT   420
TCCGCTGCGG CTCTTTACCG CCTTGGCGCT AAGCATCTGC GAGCCGCGTG GATGGACAAT   480
CTGCGCTTGG CATTCGGCCC GGGCTTGGAA ATCGGGCTTG GAGGAATTTA TAGTACACGC   540
AACGGCAATA ATCCTGCGAC ATTGAAGCTC TACACCAATG CCATCGCCCA AGCCTCGATA   600
GGATACTACG TCCCCTCCGA AACTTTTCCC CTGTATTTTC GGTTGCTCTC CCAGATCAAT   660
CTCTTCGGTA TAGCCTATGG AAATGGTTTT GGTGAGAGCT ATTACGAGAA TTTTTTGCTC   720
AATAACGGCA TTGCAGGCTC CCTGCATTTC ACTTATCCGG GCAAGTTTAC TCGGTTCACG   780
ACACTCATAA CGGCGGATAT TCCCATTCGG AACTTCTGTA CGCTTCGTGT CGGTTATCGC   840
TATTCCCATT TGGGCTCTTC GCTTAACGCA TTGGATACTC GAATCCACAG TCATACGGCT   900
TTTATCGGTT TCGTCACGGA GTTTTACCGA TTCCGTGGGC GCAAAGCCAT GAATACCGGT   960
CGGAGAACCA GTCTTTACTA TCATGAT                                        987
```

(2) INFORMATION FOR SEQ ID NO:43

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2442 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...2442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

CCCCGTTTTC ATCCCGGAGG GACACACGCT CAGCTTTGCA GAAATGGGAG AAGAAACCAA 60
AAATCAAATC AGTCATCGTG CTTTGGCGGT GGCACAGCTC CGCGATTTTT TATTATGTGC 120
AAAATAAGAT TCAGCCTCTT GCAGGCTCTT GTCGTCTGCT TATTGTTCAC CTCTTTTTCT 180
CTCCAAGCTC AAGAGGAAGG TATTTGGAAT ACCCTCTTGG CTATCCACAA GACGGAAAAA 240
GCCGTAGAAA CGCCCAAGAA AGTCTTTGCC GTAGCCAACG GAGTACTTTA CTCGGTGGGC 300
AAAGAAGCTC CCCATGAGGC AAAGATCTTC GACCGTATCA GCGGACTCAG CGATACATCG 360
GTAAGCAGCA TAGCCTACTC CGAGCAACTA AAATCCTTGG TCATATACTA TGCATCAGGC 420
AATATCGACA TCTTGGACGA AGCAGGCCGT GTGACCAACG TACCTGCATT GAAAGACAAT 480
ATCGATCTGA TAGACAAAAC GCTCAATCGC CTTTTGATCG TAGGCAACAG GGCTTATTTG 540
GCAGGAGGAT TCGGCCTCTC CGTTCTGGAT GTCGCCGAAG CTCGCATACC GGCTACCTAC 600
GCCAAGGGAA CTAAGGTGAC CGATGTGGCT AAGTTGGACA ATGATCGCTT GCTGATGCTG 660

```
AAAGAAGGGC AGCTCTTCAT CGGAAAAGAG ACCGATAACC TGCAAGATCC GGCCGCATGG     720
ACAGCCTTGT CTTTGAATTT GCCGATGGGC TCGGTCACCG GTCTGGGCAT TGTCGGGGAA     780
GACATCTGTT TCCTGCTCGC CGATGGCCGT GTATATGTCG CTGCAAACCA ATCGTTTGAG     840
CCGGAGCTAT TGCTCTCTTC CTCCGCCGAT TCACGACTGT ATGTGACGGA TCGTGGTCTG     900
TTCATCTGTG CCGAGAATCG AATTTATTTC ATAGAAAAAG GTCGCAAAAC GACACAATTT     960
CCTATAGCCG ACGTCCTTGG TGTCGGTGCC ATGAACGAAA GCAATACGGC ATACATAGCA    1020
TTGGGAGAAG AAGGTTTGGC TTCACTTCTT CTCGCAGAGG GAAGTACGGC CGAAGCCATG    1080
CCTGTAGCAT TCGACGGACC GGGGGACAAT GATTTCTACG AGATGCGGTT TAGTCACGGA    1140
CGTCTGTATG CAGCCAGCGG ACTCTGGGGA ACAAACCTGA TGGGACATGC CGGTATGGTG    1200
AAGCTATACG ACGGCAACCG ATGGACTAAC TTCGACAAGA AGACCGTACA GGAACAGTTG    1260
GGCGGCGGAT TCAGTTTCAA TGATGCTATC GATATAGCTG TTTCCAACGG AGACCCCGAT    1320
CACTTTTTTG TCGGTACATG GGGAAACGGT CTGTTCGAAT TCAAGGATGG CAAAGCGATA    1380
GCTCGCTATT CGGGAAACGA AACTGCTATC GCAGAATGTA ATCCCGGAGA TGCCCGTGTG    1440
AAAGCGATTG CCTTTGACAA TAAGGGCAAC CTCTGGGGGA CGCTCGGTGC CGTAGGCAAG    1500
AACATCTTCA TGTACGATCC GCAGAGTAGC ACATGGCATT CTTTCAGCTA TCCGGATGTA    1560
GCCAATCTGG CCTCCTTCGG CAATATGATT ATCCTACCCA ACGGAGACAA ATGGGTAAAT    1620
ATCCTTCACC GTAGTGGCGG ATCCACGCGC AAAGGTGTCT TGATCTTCAA CGATCGGGGT    1680
ACACCGGAAA CGACTTCGGA CGACAGCCAT CTTTACGTCG AGCAGTTTGT CAATCGCCTC    1740
GGGGCAGCCA TAGGACATAA GACTATCTAT GCAATGGCCG TCGATCATAA CGGCTCTGTC    1800
TGGATGGGAT CGGATATAGG CATTTTCGGC GTCTACAATG CAGCCGGAGT ATTGTCCTCG    1860
ACTTCTACCC CTATCGCTGT TCGGCCGGTC GGAGGAGAAG AACCCAATTT GTACTATGTG    1920
CTGGACAAGG TGACGGTGAC AGACATCGTC GTGGACAAAC TCAATCACAA ATGGGTTGCC    1980
ACCCAAGGGA CAGGACTCTA TCTCCTTTCG GAAGATTGCA GTAAGATCCT CGCGCAATTT    2040
ACCGTAGAAA ACAGCCCTTT GCTTTCTAAC AACATACTAT CCCTGGCCTT AAATGACGAT    2100
AACGGACTGC TGTACATCGG TACGGCGGAC GGACTGATGA CGTTCCAAAC GGGTACGGGG    2160
AGTGGATCAG CTTCCGAACT GGACGGCGTC TATGTATACC CCAATCCGCT AAGGCCGGAA    2220
TATCCCGATG GCGTCACCAT TGCCGGACTG CAAGCCGGCT GTAGTGTCAA AATCACCGAT    2280
ACCACCGGCA GACTGCTATA CCAGACTGAG AGCGTAACCA CCGAAGTCAA ATGGAATGCT    2340
CGAGGTGCCG ATGGCAATAG GGTAGCTTCG GGCGTATATG CCGTTGCAGT GTACGATCCG    2400
GTATCGAAAA AGTCCAAACT AATTCGCTTC GCAGTGATTC GC                       2442
```

(2) INFORMATION FOR SEQ ID NO:44

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1353 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

```
AAAACATCAT ATCGGAATAA TATGCGTTTC CAACATTATC TCATCTGTAC GGCTGCCGTA     60
GCGGCTTTGG CTGCGAATCC CCTTACGGGC CAATCGAATA TGACCCTCGA AGAGTGCATA    120
GACTATGCAC GCCGGCACAG TTCGGCCGTG GCGCTGTCCG CTGCGGAACT GGAGCAGTCC    180
AAGGCCGATT ACCTTCAGGC CGTCGGCAAT TTTCTGCCCC GTGTATCGGC CGGAACCGGT    240
GCTTCGTGGA ATTTCGGACG CGGATTGGAT GCCGAGACGA ATACCTACAG CGACATCAAC    300
AGCTTCAACA ATTCGTACAG CATACATGCC ACGATGACCC TTTTCGACGG TTTGCAGAGT    360
GTCTATCGAC TGCGGATGGC GCATGCACGC CGGGAGGCTT CGCGCCTCTC CGTTCGCGAG    420
CAGCAGGAGC TGGCAGCTCT CGGCACCACG GAGGCCTACT ACGACCTCGT CTATGCGCGC    480
CAAATGCAAG AGCTGGCCAT GCAGAAGTAC GAGGAGAGCA GCCGCCTCCA CCGGCAGACG    540
GCTCGAATGG AAGAGCTGGG GATGAAGAGT CGTCCCGATG TCCTCGAGAT GCAGTCGCGA    600
ATGGCCGGTG ACCGTTTGGC CCTGACTCAA GCGGACAATC AGTGCATCAT CGCTCTGATC    660
CGGCTCAAAG AAAAAATGAA CTTCCCCATC GATGACGAAC TCGTCGTAGA CGATATGCCG    720
GCTGACAGTC TCTCCGCCGA CATGGCCGAA TCGGACAGCT CGGCCGGCGT CTTCGCCCGT    780
GCTGCCCATC ATCATCCCGT CCTCCTCCGT GCCAAACTCG ACGAGCAGGC TGCCACCGAC    840
CGTTTGCGAG CCGCGCGAGG TGCATTCCTG CCGAGTGTGT CGGTATCCGG AGGATGGAAC    900
ACGGGATTCT CACGCTTTTT GAATGGATCG GACTATACGC CCTTCAGCGA GCAGTTTCGG    960
AACCGTCGGG GGGAATACGT CAGTCTGAAT CTGAGTATCC CCATCTTTTC GGGATTCAGC   1020
```

```
CTTGTGAGCC ATCTGCGTCA GGCGCGTGCC GAACGCAGGG CGGCAATCGT CCGACGGGGC     1080
GAAGCGGAGC GCAGGCTCTA CAGCGAGATC GCCCAAGCCA TGGCCGACCG GGATGCCGCT     1140
CTGGCTTCCT ACCGCCAGGC GAAGGAGCAT ACCGACGCCA TGCAAACCGC TTACGAAGCC     1200
GTCTTGCAGC GTTATGAGGA GGGGCTGAAT ACGGCCATCG ACCTGACCAC TCAGGCCAAT     1260
CGGCTCCTGG ATGCCCGTGT GCAGCGACTG AGAGCGGCCA TGACCTACCG GCTCAAATGC     1320
AAACTCATAG CCTATTACGG CTGCCTTTCG GAC                                  1353
```

(2) INFORMATION FOR SEQ ID NO:45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 589 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

```
Asp Tyr Gln Ile His Glu Gly Ala Tyr Ile Ile Pro Val Lys Glu Gln
1               5                   10                  15
Met Arg Pro Leu Phe Asn Gly Asn Asn Asn Phe Ser Ile Tyr Val Val
            20                  25                  30
Ala Asn Leu Asp Phe Asn Ala Pro Ala Thr Glu Ala Ala Leu Ser Gln
        35                  40                  45
Phe Val Val Glu Lys Ser Ile Glu Val Ser Ser Thr Thr Ala Pro Ala
```

```
    50                  55                  60
Asp Phe Val Met Leu Ala His Gly Asn Lys Gln Ile Asn Met Ala Thr
65                  70                  75                  80
Thr Glu Gly Lys Leu Leu Gly Asp Tyr Lys Leu Lys Arg Val Ala Ala
                85                  90                  95
Lys Ile Arg Met Ile Lys Pro Thr Ile Asn Val Gln Gly Tyr Glu Val
            100                 105                 110
Val Gly Asn Ile Gln Ala Lys Phe Arg Asn Ser Val Thr Lys Gly Phe
        115                 120                 125
Leu Thr Thr Glu Ala Gln Glu Ile Pro Ala Ala Ala Ser Tyr Lys Thr
    130                 135                 140
Ser Glu Tyr Leu Asp Ile Ala Glu Ser Ala Pro Ala Asn Ser Ile His
145                 150                 155                 160
Phe Tyr Ser Tyr Tyr Asn Lys Trp Thr Leu Ser Thr Pro Glu Lys Arg
                165                 170                 175
Pro Glu Phe Phe Ile Met Val Lys Phe Lys Lys Thr Gly Gln Pro Asp
            180                 185                 190
Asn Thr Ala Lys Pro Tyr Tyr Tyr Arg Val Pro Leu Glu Ser Gln Asp
        195                 200                 205
Asn Gln Val Lys Ser Asn Val Leu Tyr Asn Leu Asn Val Lys Ile Glu
    210                 215                 220
Ile Leu Gly Ser Leu Gln Glu Pro Glu Ala Val Ser Val Asn Gly Thr
225                 230                 235                 240
Leu Ala Ile Glu Glu Trp Ile Leu His Gln Asp Ala Phe Asn Leu Pro
                245                 250                 255
Ala Thr Asn Tyr Leu Ile Val Glu Gln His Glu Ile Phe Met Asn Asn
            260                 265                 270
Val Asn Thr Tyr Ser Val Lys Tyr Gln Thr Ser Gln Lys Pro Ile Ser
        275                 280                 285
Ile Ser Ile Gln Ser Val Thr Phe Ser Tyr Val Ser Ser Asp Gly Thr
    290                 295                 300
Gln His Asn Asp Leu Val Ala Ser Ser Ser Asp Gln Tyr Pro Thr Ile
305                 310                 315                 320
Thr Ser Asp Asn Thr Ser Ile Ile Ile Thr Ser Lys Ile Pro Val Asn
                325                 330                 335
Asn Val Pro Lys Lys Ile Val Phe Glu Val Thr Asn Gly Val Ala Gly
```

```
            340                 345                 350
Leu Lys Glu Thr Val Thr Val Leu Gln Tyr Pro Ala Gln Phe Ile Val
        355                 360                 365
Asn Thr Leu Gly Thr Ala Ser Ala Trp Arg Pro Asp Gly Ser Leu Ala
    370                 375                 380
Pro Gly Leu Asn Asn Lys Ala Ile Tyr His Val Val Val Leu Val Pro
385                 390                 395                 400
Pro Glu Asn Leu Phe Glu Asp Gly Thr Gln Thr Ile Ile Gly Tyr Pro
                405                 410                 415
Pro Thr Glu Thr Ile Ser Phe His Lys Lys Glu Asn Asn Thr Tyr Pro
            420                 425                 430
Ile Val Trp Ser Asp Thr Asn Thr Thr Lys Gln Asp Leu Glu Thr Ser
        435                 440                 445
Arg Met Ile Ser Pro Ser Phe Glu Leu Ala Ser Gln Leu Gly Ala Thr
    450                 455                 460
Leu Pro Met Pro Tyr Leu Glu Tyr Trp Pro Gly Thr Ser Tyr Leu Leu
465                 470                 475                 480
Asp Tyr Ser Gly Asn Tyr Asn Asn Lys Arg Tyr Ala Leu Phe Asn Cys
                485                 490                 495
Ala Phe Tyr Trp Glu Lys Arg Lys Val Asn Asn Glu Glu Ile Lys Phe
            500                 505                 510
Asp Asp Trp Arg Leu Pro Thr Glu Ala Glu Ile Lys Leu Ile Asp Lys
        515                 520                 525
Leu Gln His Asn Glu Gln Ser Ala Val Gln Ala Ile Met Thr Gly Asn
    530                 535                 540
Tyr Tyr Trp Asp Ser Tyr Ser Ala Asn Gly Ser Tyr Lys Met Gln Gly
545                 550                 555                 560
Gly Gly Gly Gln Gly Asn Ser Ser Lys Ala Tyr Val Arg Cys Val Arg
                565                 570                 575
Asp Val Lys Lys Pro Ile Arg Asp Lys Lys Ser Gly Lys
            580                 585
```

(2) INFORMATION FOR SEQ ID NO:46

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 907 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

```
Thr Ile Cys Val Ala Phe Leu Ser Ala Pro Val Ala Ala Leu Arg Glu
1               5                   10                  15
Ser Pro Pro Met Gly Ala Glu Arg Lys Thr Pro Ser Leu Leu Pro Leu
            20                  25                  30
Leu Phe Glu His Ser Asp Lys Gly Lys Gly Phe Asp Tyr Arg Leu Phe
        35                  40                  45
Thr Ser Asn Lys Leu Lys Val Phe Ala Thr Gly Asn Ser Arg Tyr Ile
    50                  55                  60
His Asn Lys Pro Thr Ile Ile Gln Ala Met Lys Arg Ile Val Leu Ser
65                  70                  75                  80
Ser Phe Leu Phe Val Leu Ser Ile Leu Ser Leu Met Ala Gln Asn Asn
                85                  90                  95
Thr Leu Asp Val His Ile Ser Gly Thr Ile Lys Asp Ala Ser Ser Gly
            100                 105                 110
Glu Pro Val Pro Tyr Ala Thr Val Ser Ile Arg Leu Thr Gly Ala Asp
        115                 120                 125
Thr Thr Gln Val Phe Arg Gln Val Thr Asp Gly Asn Gly Tyr Phe Val
    130                 135                 140
Ile Gly Leu Pro Ala Ala Pro Ser Tyr His Leu Thr Ala Ser Phe Val
145                 150                 155                 160
```

```
Gly Met Lys Thr His Thr Met Gln Ile Ser Arg Gly Asn Gly Gln His
                165                 170                 175
Asp Ile Lys Ser Ile Asp Ile Ser Leu Glu Ser Glu Asp Lys Gln Leu
            180                 185                 190
Ser Thr Val Thr Val Ser Ala Ala Arg Pro Leu Val Lys Met Glu Ile
        195                 200                 205
Asp Arg Leu Ser Tyr Asn Met Lys Asp Asp Pro Ala Ala Lys Thr Asn
    210                 215                 220
Asn Leu Leu Glu Met Leu Arg Asn Val Pro Leu Val Thr Val Asp Gly
225                 230                 235                 240
Gln Gly Asn Ile Gln Val Lys Gly Ser Ser Asn Phe Lys Ile His Leu
                245                 250                 255
Asn Gly Arg Pro Ser Thr Met Val Ser Ser Asn Pro Lys Glu Val Phe
            260                 265                 270
Arg Ser Ile Pro Ala His Thr Ile Lys Arg Val Glu Val Ile Thr Asp
        275                 280                 285
Pro Gly Val Lys Tyr Asp Ala Glu Gly Thr Ser Ala Ile Leu Asp Ile
    290                 295                 300
Val Thr Glu Glu Gly Lys Lys Leu Glu Gly Tyr Ser Gly Ser Ile Thr
305                 310                 315                 320
Ala Ser Val Ser Asn Asn Pro Thr Ala Asn Gly Ser Ile Phe Leu Thr
                325                 330                 335
Ala Lys Ser Gly Lys Val Gly Leu Thr Thr Asn Tyr Asn Tyr Tyr Gly
            340                 345                 350
Gly Lys Asn Lys Gly Ser Arg Tyr Phe Thr Glu Arg Thr Thr Ser Met
        355                 360                 365
Leu Gln Thr Ile Glu Glu Gly Lys Gly Gln Glu Thr Phe Gly Gly His
    370                 375                 380
Phe Gly Asn Ala Leu Leu Ser Phe Glu Ile Asp Ser Leu Asn Leu Phe
385                 390                 395                 400
Thr Val Gly Gly Asn Val Arg Leu Trp Glu Met Thr Thr Asp Arg Asn
                405                 410                 415
Ser Val Glu Lys Ser Phe Ala Gly Ser Asn Leu Met Ser Tyr Ile Asp
            420                 425                 430
Arg Lys Leu Lys Thr Gln Met Asp Ala Gly Ser Tyr Glu Leu Asn Ala
        435                 440                 445
```

Asp Tyr Gln His Ser Thr Arg Leu Pro Gly Glu Leu Leu Thr Val Ser
450 455 460

Tyr Arg Phe Thr His Asn Pro Asn Asn Ser Glu Thr Phe Ile Asp Gln
465 470 475 480

Trp Lys Arg Asp Pro Leu Asn Thr Ala Asn Thr Ile Gln Tyr Ala Gly
485 490 495

Gln His Ser Lys Ser Asp Ala Gly Met Asp Glu His Thr Ala Gln Val
500 505 510

Asp Tyr Thr Arg Pro Leu Gly Gln Ala His Ser Leu Glu Ala Gly Leu
515 520 525

Lys Tyr Ile Tyr Arg His Ala Thr Ser Asp Pro Leu Tyr Glu Ile Arg
530 535 540

Pro Ser Glu Asp Ala Pro Trp Gln Pro Gly Ser Leu Tyr Ala Gln Asn
545 550 555 560

Pro Ser Asn Gly Lys Phe Arg His Asp Gln Tyr Ile Gly Ala Ala Tyr
565 570 575

Ala Gly Tyr Asn Tyr Arg Lys Asp Gln Tyr Ser Leu Gln Thr Gly Leu
580 585 590

Arg Val Glu Ser Ser Arg Leu Lys Ala Leu Phe Pro Glu Asn Ala Ala
595 600 605

Ala Asp Phe Ser His Asn Ser Phe Asp Trp Val Pro Gln Leu Thr Leu
610 615 620

Gly Tyr Thr Pro Ser Pro Met Lys Gln Leu Lys Leu Ala Tyr Asn Phe
625 630 635 640

Arg Ile Gln Arg Pro Ala Ile Gly Gln Leu Asn Pro Tyr Arg Leu Gln
645 650 655

Thr Asn Asp Unk Gln Val Gln Tyr Gly Asn Pro Asp Leu Lys Ser Glu
660 665 670

Lys Arg His His Val Gly Leu Ser Tyr Asn Gln Tyr Gly Ala Lys Val
675 680 685

Met Leu Thr Ala Ser Leu Asp Tyr Asp Phe Cys Asn Asn Ala Ile Gln
690 695 700

Asn Tyr Thr Phe Ser Asp Pro Ala Asn Pro Asn Leu Phe His Gln Thr
705 710 715 720

Tyr Gly Asn Ile Gly Arg Glu His Ser Phe Ser Leu Asn Thr Tyr Ala
725 730 735

Met Tyr Thr Pro Ala Val Trp Val Arg Ile Met Leu Asn Gly Asn Ile
740 745 750

Asp Arg Thr Phe Gln Lys Ser Glu Ala Leu Gly Ile Asp Val Asn Ser
755 760 765

Trp Ser Gly Met Val Tyr Ser Gly Leu Met Phe Thr Leu Pro Lys Asp
770 775 780

Trp Thr Val Asn Leu Phe Gly Gly Tyr Tyr His Gly Gly Arg Ser Tyr
785 790 795 800

Gln Thr Lys Tyr Asp Gly Asn Val Phe Asn Asn Ile Gly Ile Ala Lys
805 810 815

Gln Leu Phe Asp Lys Lys Leu Arg Val Ser Leu Ser Ala Asn Asn Ile
820 825 830

His Ala Lys Tyr Ser Thr Trp Lys Ser Arg Thr Ile Gly Asn Gly Phe
835 840 845

Thr Ile Tyr Ser Glu Asn Ala Gly Ile Gln Arg Ser Val Ser Leu Ser
850 855 860

Leu Thr Tyr Ser Phe Gly Lys Met Asn Thr Gln Val Arg Lys Val Glu
865 870 875 880

Arg Thr Ile Val Asn Asp Asp Leu Lys Gln Thr Ser Ser Gln Gly Gln
885 890 895

Gln Gly Gly Gly Gln Gly Asn Pro Thr Gly Asn
900 905

(2) INFORMATION FOR SEQ ID NO:47

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 606 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

```
Ile Ile Phe Cys Thr Ile His His Ser Glu Leu Glu Ile Met Asn Ser
1               5                   10                  15
Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val
            20                  25                  30
Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro
        35                  40                  45
Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu
    50                  55                  60
Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro
65                  70                  75                  80
Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe
                85                  90                  95
Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu
            100                 105                 110
Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile
        115                 120                 125
Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp
    130                 135                 140
Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys
145                 150                 155                 160
Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg
                165                 170                 175
Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu
            180                 185                 190
Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg
        195                 200                 205
Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val
    210                 215                 220
Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly
```

```
225                 230                 235                 240
Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg
                245                 250                 255
Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His
            260                 265                 270
Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile
        275                 280                 285
Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn
    290                 295                 300
Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu
305                 310                 315                 320
Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp
                325                 330                 335
Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe
            340                 345                 350
Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu
        355                 360                 365
Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val
    370                 375                 380
Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu
385                 390                 395                 400
Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln
                405                 410                 415
Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr
            420                 425                 430
Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu
        435                 440                 445
Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu
    450                 455                 460
Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu
465                 470                 475                 480
Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly
                485                 490                 495
Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu
            500                 505                 510
Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val
```

515 520 525

Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly

530 535 540

Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser

545 550 555 560

Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys

565 570 575

Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro

580 585 590

Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe

595 600 605

(2) INFORMATION FOR SEQ ID NO:48

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

Asn Ser His Ala Thr Val Ser Val Ile Cys Ser Met Met Glu Lys Cys

1 5 10 15

Ile Phe Ala His Tyr Pro His Asn Leu Val Phe Met Ile Arg Lys His

20 25 30

```
Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val Phe Ser Ala Gly Ala
        35                  40                  45
Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn Leu Pro Ala Thr Ala
    50                  55                  60
Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr Ile Val Asp Asp Asn
65                  70                  75                  80
Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu Gly Tyr Glu Ser Gly
                85                  90                  95
Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met Ser Gly Ser His Met
            100                 105                 110
Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu Arg Gly Met Trp Gly
        115                 120                 125
Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met Gln Gly Tyr Asp Gln
    130                 135                 140
Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser Asp Ile Ala Val Gln
145                 150                 155                 160
Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe Arg Gly Gly Val Ser
                165                 170                 175
Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr Ser Ser Phe Gly Leu
            180                 185                 190
Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp Asp Lys Gly Tyr Ser
        195                 200                 205
Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln Leu Lys Gly Tyr Asn
    210                 215                 220
Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln Leu Gly Phe Ser Arg
225                 230                 235                 240
Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile Thr Leu Phe Asn Leu
                245                 250                 255
Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg Asp Leu Ser Lys Met
            260                 265                 270
Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala Glu Phe Thr Pro Ser
        275                 280                 285
Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro Gln Ile Ala Gln Asp
    290                 295                 300
Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly Leu Ser Ala Gly Val
305                 310                 315                 320
```

```
Gly Phe Thr Ser Gly Val Val Arg Val Gly Val Ser Ala Ala Thr Tyr
                325                 330                 335
His Pro Ala Ala Leu Ser Phe Met Cys Ser Val Gly Ile Arg Leu Asp
            340                 345                 350
Asp Lys Ser Ile Phe
        355
```

(2) INFORMATION FOR SEQ ID NO:49

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

```
Lys Phe Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu
1               5                   10                  15
Phe Ser Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg
            20                  25                  30
Ser Tyr Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val
        35                  40                  45
Pro Pro Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly
    50                  55                  60
Leu Pro Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly
```

```
65                  70                  75                  80
Asp Ile Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn
                85                  90                  95
Glu Trp Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly
            100                 105                 110
Arg Phe Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys
        115                 120                 125
Thr Arg Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu
    130                 135                 140
Ile Pro Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro
145                 150                 155                 160
Cys Ile Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp
                165                 170                 175
Asp Thr Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys
            180                 185                 190
Pro Phe Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln
        195                 200                 205
Lys Tyr Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala
    210                 215                 220
Gln Thr Val Ser Gln Gln Lys
225                 230
```

(2) INFORMATION FOR SEQ ID NO:50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 566 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

```
Tyr Asp Gly Ala Arg Leu Val Tyr Thr Leu Phe Arg Asn Arg Asn Asp
1               5                   10                  15
Ile His Pro Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala
            20                  25                  30
Leu Phe Phe Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln
        35                  40                  45
Met Leu Asn Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro
    50                  55                  60
Thr Glu Arg Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg
65                  70                  75                  80
Gly Ala Asp Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr
                85                  90                  95
Val Arg Phe Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro
            100                 105                 110
Tyr Asn Gly Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg
        115                 120                 125
Ile Ser Val Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser
    130                 135                 140
Arg Gly Met His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu
145                 150                 155                 160
Ala Tyr Tyr Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His
                165                 170                 175
Phe Glu Asp Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg
            180                 185                 190
Leu Pro Leu Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg
        195                 200                 205
Leu Thr Asp Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser
    210                 215                 220
Cys Ala Thr Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser
225                 230                 235                 240
```

```
Ala Ala Tyr Leu Tyr His Arg Gln His Leu Thr Gln Tyr Asn Trp Arg
                245                 250                 255
Pro Gly Gln Gln Asp Lys Phe Phe Val Ser Tyr Gly Phe Gly Gln Val
            260                 265                 270
Asp Val Ser Asn Ser Pro Ile Trp Phe Gly Ile Ser Arg Met Asn Tyr
        275                 280                 285
Val Asn Gly Trp Lys Leu Ser Ser Arg Leu Asp Thr Arg Arg Gly Asp
    290                 295                 300
Ala Ile Gly Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg
305                 310                 315                 320
Ser Ser Ile Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr
                325                 330                 335
Gly Ser Trp His Leu Ser Asp Phe Asp Phe Ser Phe Ser Ala Asp Tyr
            340                 345                 350
Ala Leu Arg Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp
        355                 360                 365
Asp Asn Tyr His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp
    370                 375                 380
Tyr Met Leu Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile
385                 390                 395                 400
Arg Thr Asp Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe
                405                 410                 415
Tyr Gly Tyr Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser
            420                 425                 430
Gly Met Leu Arg Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser
        435                 440                 445
Lys Leu Asp Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu
    450                 455                 460
Thr His Ser Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr
465                 470                 475                 480
Gln Leu Ala Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu
                485                 490                 495
Val Arg Ser Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg
            500                 505                 510
Leu Met Thr Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp
        515                 520                 525
```

Gly Ile Ala Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser
530 535 540

Asp Pro Gln Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys
545 550 555 560

Asn Ile Ser Tyr Leu Phe
565

(2) INFORMATION FOR SEQ ID NO:51

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

Arg Thr Asn Val Phe Leu Ser Leu Ser His Lys Ile Gly Arg Arg Gly
1 5 10 15

Ala Ser Cys Ser Asn Arg Asn Ala Trp Met Ala Glu Asn Lys Pro Ser
20 25 30

Ser Pro Glu Pro Asp Asn Thr Gly Val Gly Asn Ser Pro Ser Asp Tyr
35 40 45

Leu His Gly Glu Ala Ile Ile Pro Pro Leu Ser Ser Leu Ser Asn Phe
50 55 60

Asn Asp Lys Arg Phe Met Lys Lys Leu His Met Ile Ala Ala Leu Ala

```
65                  70                  75                  80
Val Leu Pro Phe Cys Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu
                85                  90                  95
Ile Asp Ser Leu Ser Asn Val Gln Leu Gln Thr Val Gln Val Val Ala
            100                 105                 110
Thr Arg Ala Thr Ala Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys
        115                 120                 125
Ala Glu Leu Ser Lys Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu
    130                 135                 140
Met Leu Thr Pro Ser Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile
145                 150                 155                 160
Gly Tyr Ser Gly Phe Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn
                165                 170                 175
Ile Thr Thr Asn Gly Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val
            180                 185                 190
Phe Trp Val Asn Met Pro Asp Phe Ala Ser Ser Ile Glu Asp Leu Gln
        195                 200                 205
Val Gln Arg Gly Val Gly Thr Ser Thr Asn Gly Ala Gly Ala Phe Gly
    210                 215                 220
Ala Ser Val Asn Met Arg Thr Asp Asn Leu Gly Leu Ala Pro Tyr Gly
225                 230                 235                 240
Arg Val Asp Leu Ser Gly Gly Ser Phe Gly Thr Phe Arg Arg Ser Val
                245                 250                 255
Lys Leu Gly Ser Gly Arg Ile Gly Arg His Trp Ala Val Asp Ala Arg
            260                 265                 270
Leu Ser Lys Ile Gly Ser Asp Gly Tyr Val Asp Arg Gly Ser Val Asp
        275                 280                 285
Leu Lys Ser Tyr Phe Ala Gln Val Gly Tyr Phe Gly Ser Asn Thr Ala
    290                 295                 300
Leu Arg Phe Ile Thr Phe Gly Gly Lys Glu Val Thr Gly Ile Ala Trp
305                 310                 315                 320
Asn Gly Leu Ser Lys Glu Asp Glu Ala Lys Tyr Gly Arg Arg Tyr Asn
                325                 330                 335
Ser Ala Gly Leu Met Tyr Val Asp Ala Gln Gly Val Pro His Tyr Tyr
            340                 345                 350
His Asn Thr Asp Asn Tyr Glu Gln Arg His Tyr His Ala Ile Met Thr
```

355 360 365

His Ser Phe Ser Pro Ser Val Ile Leu Asn Leu Thr Ala His Tyr Thr

370 375 380

Ala Gly Tyr Gly Tyr Thr Asp Glu Tyr Arg Thr Gly Arg Lys Leu Lys

385 390 395 400

Glu Tyr Ala Leu Gln Pro Tyr Val Glu Asn Ser Val Thr Val Lys Lys

405 410 415

Thr Asp Leu Ile Arg Gln Lys Tyr Leu Asp Asn Asp Phe Gly Gly Leu

420 425 430

Ile Gly Ser Leu Asn Trp His Thr Gly Ala Trp Asp Leu Gln Phe Gly

435 440 445

Ala Ser Gly Asn Ile Tyr Lys Gly Asp His Phe Gly Arg Ile Thr Tyr

450 455 460

Ile Lys Lys Tyr Asn Gln Pro Leu Ala Pro Asp Phe Glu Tyr Tyr Arg

465 470 475 480

Asn Arg Ala Asp Lys Arg Glu Gly Ala Ala Phe Ala Lys Ala Asn Trp

485 490 495

Gln Ile Thr Pro Glu Leu Asn Met Tyr Ala Asp Leu Gln Tyr Arg Thr

500 505 510

Ile Gly Tyr Thr Ile Asn Gly Ile Thr Asp Glu Tyr Asp Glu Val Gln

515 520 525

Gly Ser Met Gln His Ile Asp Leu Asp Lys Thr Phe Arg Phe Leu Asn

530 535 540

Pro Lys Ala Gly Leu Thr Tyr Ser Phe Asp Asp Ala His Thr Ala Tyr

545 550 555 560

Ala Ser Val Ala Val Ala His Arg Glu Pro Asn Arg Thr Asn Tyr Thr

565 570 575

Glu Ala Gly Ile Gly Gln Tyr Pro Thr Pro Glu Arg Leu Ile Asp Tyr

580 585 590

Glu Leu Gly Tyr Arg Tyr Ala Ser Pro Leu Leu Ser Ala Gly Val Gly

595 600 605

Leu Tyr Tyr Met Gln Tyr Lys Asp Gln Leu Val Leu Asp Gly Arg Leu

610 615 620

Ser Asp Val Gly Gln Met Leu Thr Ser Asn Val Pro Asp Ser Tyr Arg

625 630 635 640

Met Gly Leu Glu Leu Thr Leu Gly Trp Gln Ile Leu Pro Arg Leu Leu

```
                645                 650                 655
Arg Trp Asp Ala Ser Phe Thr Met Ser Arg Asn Lys Ile Asp Arg Tyr
            660                 665                 670
Val Gln Tyr Thr Ser Val Tyr Asp Ala Asp Tyr Asn Trp Leu Glu Leu
        675                 680                 685
Lys Glu Glu Thr Leu Glu Ser Thr Asp Ile Ala Tyr Ser Pro Asn Val
    690                 695                 700
Ile Ala Gly Ser Met Leu Thr Leu Ser His Ala Gly Phe Glu Met Ala
705                 710                 715                 720
Trp Thr Ser Arg Phe Val Ser Lys Gln Tyr Leu Asp Asn Thr Gln Arg
                725                 730                 735
Ser Asp Arg Met Leu Ser Ser Tyr Trp Val Asn Asp Leu Arg Leu Gly
            740                 745                 750
Tyr Val Leu Pro Val His Phe Val Lys Arg Val Ala Leu Gly Val Gln
        755                 760                 765
Leu Asn Asn Leu Phe Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr
    770                 775                 780
Asp Ala Gly Tyr Val Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp
785                 790                 795                 800
Leu Arg Tyr Tyr Pro Gln Ala Gly Phe Asn Ala Leu Gly Unk Leu Thr
                805                 810                 815
Ile Asp Phe
```

(2) INFORMATION FOR SEQ ID NO:52

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 319 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

```
Phe Thr Ser Gly Thr Ile Phe Val Arg Ile Ala Ile Ser Gly Arg Val
1               5                   10                  15
Val Cys Arg Glu Val Glu Asp Asn Gly Arg Arg Glu Ala Val Arg His
            20                  25                  30
Asp Gly Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val
        35                  40                  45
Val Arg Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val
    50                  55                  60
Ser Ala Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys
65                  70                  75                  80
Asp Thr Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg
                85                  90                  95
Val Ala Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His
            100                 105                 110
Ala Ser Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly
        115                 120                 125
Ile His Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg
    130                 135                 140
Ser Ala Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile
145                 150                 155                 160
Arg Ser Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys
                165                 170                 175
Ser Ser Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys
            180                 185                 190
Val Phe Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly
        195                 200                 205
Leu Arg Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp
    210                 215                 220
```

```
Ala Ile Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr
225                 230                 235                 240
Arg Thr Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln
                245                 250                 255
Ile Gly Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala
            260                 265                 270
Asn Val Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr
        275                 280                 285
Asp Leu Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala
    290                 295                 300
Val Gly Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly
305                 310                 315
```

(2) INFORMATION FOR SEQ ID NO:53

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

```
Ser Thr Ile Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu
1               5                   10                  15
Gly Leu Cys Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly
```

20 25 30

His Ser Ile Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr

35 40 45

Val Glu Asn Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile

50 55 60

Asp Met Asp Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile

65 70 75 80

Ser Arg Glu Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu

85 90 95

Tyr Asn Gly Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu

100 105 110

Ile Gly Ala Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe

115 120 125

Thr Ile Thr Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr

130 135 140

Tyr Gln Ile Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu

145 150 155 160

Thr Phe Asn Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro

165 170 175

Ile Gly Gly Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser

180 185 190

Glu Pro Gln Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys

195 200 205

Asp Phe Asn Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe

210 215 220

Ala Arg Met Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp

225 230 235 240

Thr Phe Asn

(2) INFORMATION FOR SEQ ID NO:54

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
  (A) NAME/KEY: misc_feature
  (B) LOCATION 1...450

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

```
Trp Cys Gln Ser Asp Pro Ile Pro His Cys His Ala Val Tyr Arg Asn
1               5                   10                  15
Ala Gln Gly His Gln Gln Gly Arg Ser Asp Gln Asp Arg Leu Pro Pro
            20                  25                  30
Val Arg Gly Tyr Arg Tyr Ala Arg Cys Leu Gly Arg Tyr Glu Gly Phe
        35                  40                  45
Gly Glu Arg Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met
    50                  55                  60
Leu Pro Ala Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu
65                  70                  75                  80
Arg Leu Glu Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile
                85                  90                  95
Arg Ser Ala Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val
            100                 105                 110
Lys Gly Tyr Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr
        115                 120                 125
Ser Leu Pro Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr
    130                 135                 140
Leu Asn Tyr Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser
145                 150                 155                 160
Asp Leu Pro Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile
                165                 170                 175
```

```
Leu Pro Tyr Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu
            180                 185                 190
Met Leu Gly Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro
        195                 200                 205
Ile Tyr Asn Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val
    210                 215                 220
Gln Phe Arg Gly Asp Trp Thr Arg Phe Arg Met Asp Val Trp Val Asn
225                 230                 235                 240
Trp Met Ser Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val
                245                 250                 255
Phe Gly Leu Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp
            260                 265                 270
Arg Leu Glu Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu
        275                 280                 285
Tyr Asn Trp Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala
    290                 295                 300
Val Gly Leu Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln
305                 310                 315                 320
Ile Trp Gly Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr
                325                 330                 335
Phe Pro Tyr Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp
            340                 345                 350
Leu Glu His Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr
        355                 360                 365
Val Ser Pro Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys
    370                 375                 380
Gln Pro Leu Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp
385                 390                 395                 400
Tyr Ser Trp Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg
                405                 410                 415
Val Trp Phe Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu
            420                 425                 430
Leu Thr Met Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly
        435                 440                 445
Asn His
    450
```

(2) INFORMATION FOR SEQ ID NO:55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...447

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

```
Pro Phe Ser Pro Pro Trp Val Cys Ala Gly Ala Ala Ser Ser Val Arg
1               5                   10                  15
Thr Arg Pro Cys Ser Thr Val Ser Ser Thr Ala Ala Ser Ser His Arg
            20                  25                  30
Arg Ser Glu His Met Arg Ser Ala Asp Ser Ser Pro Ala Tyr Ser Pro
        35                  40                  45
Ile Gly Ser Leu Ser Ser Ser His Ser Phe Asp Ser Ile Pro Asp Gln
    50                  55                  60
Arg Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly
65                  70                  75                  80
Met Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu
                85                  90                  95
Pro Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys
            100                 105                 110
Leu Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val
```

```
        115                 120                 125
Asp Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met
    130                 135                 140
Ser Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln
145                 150                 155                 160
Arg Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser
                165                 170                 175
Asn Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val
            180                 185                 190
Ser Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr
        195                 200                 205
Asp Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr
    210                 215                 220
Met Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro
225                 230                 235                 240
Glu Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe
                245                 250                 255
Ala Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr
            260                 265                 270
Pro Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala
        275                 280                 285
Leu His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg
    290                 295                 300
Asn Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg
305                 310                 315                 320
Ile Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp
                325                 330                 335
Lys Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp
            340                 345                 350
Val Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp
        355                 360                 365
Gln Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro
    370                 375                 380
Ala Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met
385                 390                 395                 400
Gly Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val
```

```
                    405                         410                         415
Thr Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser
                420                         425                         430
Thr Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu
            435                         440                         445
```

(2) INFORMATION FOR SEQ ID NO:56

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 532 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...532

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

```
Tyr Arg Arg Ser Gly Arg Val Cys Pro Arg Ile Leu Arg Asn Lys Arg
1               5                   10                  15
Ser Tyr Ala Asp Thr Arg Leu Gln Pro Arg Arg Ala Val Arg Leu Arg
            20                  25                  30
Ala Gly Thr Arg Thr Lys Met Lys Arg Arg Phe Leu Ser Leu Leu Leu
        35                  40                  45
Leu Tyr Ile Leu Ser Ser Ile Ser Leu Ser Ala Gln Arg Phe Pro Met
    50                  55                  60
Val Gln Gly Ile Glu Leu Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys
65                  70                  75                  80
```

```
Arg Pro Trp Arg Ala Ile Gly Lys Thr Ile Gly Val Asn Leu Ala Val
                85                  90                  95
Trp Gly Phe Asp His Phe Ile Met Asn Glu Asp Phe Ala Asp Ile Ser
            100                 105                 110
Trp Gln Thr Ile Lys Ser Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn
        115                 120                 125
Asp Lys Phe Val Thr Asn Leu Phe Ala His Pro Tyr His Gly Ser Leu
    130                 135                 140
Tyr Phe Asn Ala Ala Arg Ser Asn Gly Leu Ser Phe Arg His Ser Ala
145                 150                 155                 160
Pro Phe Ala Phe Phe Gly Ser Leu Met Trp Glu Leu Leu Met Glu Asn
                165                 170                 175
Glu Pro Pro Ser Ile Asn Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile
            180                 185                 190
Ala Leu Gly Glu Met Gly His Arg Leu Ser Asp Leu Leu Ile Asp Asn
        195                 200                 205
Arg Thr Thr Gly Trp Glu Arg Met Gly Arg Glu Val Ala Ile Ala Leu
    210                 215                 220
Ile Asn Pro Met Arg Phe Leu Asn Arg Leu Thr Ala Gly Glu Val Thr
225                 230                 235                 240
Ser Val Gly Ser Arg Ser Gly Gln Ile Phe Gln Ser Val Pro Ile Asn
                245                 250                 255
Ile Val Val Asp Ala Gly Phe Arg Phe Leu Ala Asp Lys Arg His Ala
            260                 265                 270
Arg Thr Gly Ala Thr Ala Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly
        275                 280                 285
Asp Pro Phe Arg Ser Glu Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe
    290                 295                 300
Lys Ala Gly Leu Ser Phe Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile
305                 310                 315                 320
Asn Leu Ile Gly Ile Leu Ser Gly Cys Gln Leu Leu Ala His Glu Arg
                325                 330                 335
Thr Val Leu Val Gly Gly Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser
            340                 345                 350
Glu Lys Arg Ile Ser Lys Asn Ser Glu Glu Val Leu Val Thr Pro Tyr
        355                 360                 365
```

```
Arg Ile Ser Gln Val Ala Ala Leu Gly Gly Gly Leu Ile Phe Gln His
    370                 375                 380
His Gly Lys Phe Arg Arg Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr
385                 390                 395                 400
Leu Asn Val Val Pro Met Gly Ala Ser Leu Ser Asp His Tyr Asn Val
                405                 410                 415
Asp Asn Arg Asp Tyr Asn Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr
            420                 425                 430
Leu Gly Ala Thr Tyr Asn Asp Leu Trp Ser Trp Leu Leu Gly Val Glu
        435                 440                 445
Ser Tyr Arg Leu Tyr Thr Trp Ile Gly Tyr Glu Glu Pro His Gln Lys
    450                 455                 460
Asn Thr Asp Val Ser Ser Phe Met Val Gln Gly Asp Glu Ser Lys Ala
465                 470                 475                 480
Arg Leu Leu Val Thr Ser Ser Glu Phe Ala Phe His Pro Gly Pro Trp
                485                 490                 495
His Val Ala Ile Val Ala Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln
            500                 505                 510
Phe Tyr Pro Asn Val Ser Phe Asp Thr Gly Asp Ile Gln Leu Arg Val
        515                 520                 525
Gly Phe His Phe
    530
```

(2) INFORMATION FOR SEQ ID NO:57

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57

```
Lys Arg Arg Lys Lys Gln Met Lys Arg Leu Ile Val Phe Leu Ala Met
1               5                   10                  15
Gly Gly Leu Leu Phe Thr Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala
            20                  25                  30
Ser Asp Thr Pro Lys Lys Asp Trp Thr Ile Lys Gly Val Thr Gly Leu
        35                  40                  45
Asn Ala Ser Gln Thr Ser Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn
    50                  55                  60
Thr Val Ala Gly Asn Leu Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys
65                  70                  75                  80
Asp Lys Trp Ser Trp Asp Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr
                85                  90                  95
Tyr Thr Thr Ala Asn Lys Trp Asn Lys Ser Val Asp Lys Ile Glu Leu
            100                 105                 110
Phe Thr Lys Ala Gly Tyr Glu Ile Gly Lys His Trp Tyr Gly Ser Ala
        115                 120                 125
Leu Phe Thr Phe Leu Ser Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser
    130                 135                 140
Asp His Leu Thr Gly Val Lys His Ile Ser Asn Phe Phe Ala Pro Ala
145                 150                 155                 160
Tyr Leu Thr Leu Gly Ile Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe
                165                 170                 175
Ser Leu Tyr Leu Ser Pro Thr Thr Gly Lys Leu Thr Val Val Ala Asp
            180                 185                 190
Asp Tyr Leu Ser Ser Leu Gly Ala Phe Gly Val Lys Val Gly Glu Lys
        195                 200                 205
Thr Met Phe Glu Leu Gly Ala Leu Val Val Gly Ser Ala Asn Ile Asn
    210                 215                 220
Leu Met Glu Asn Val Asn Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala
```

```
225                 230                 235                 240
Tyr Thr His Asp Phe Gly Asn Ile Asp Ile Asn Trp Glu Ala Met Leu
                245                 250                 255
Ala Met Lys Ile Asn Lys Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu
            260                 265                 270
Ile Tyr Asp Asp Asp Val Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe
        275                 280                 285
Lys Glu Val Val Gly Val Gly Val Ala Tyr Thr Phe
    290                 295                 300
```

(2) INFORMATION FOR SEQ ID NO:58

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 973 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58

```
Phe Tyr Thr Gly Ile Asp Leu His Ile Glu Ser Gln Met Lys Lys Leu
1               5                   10                  15
Phe Pro Leu Leu Leu Leu Ile Leu Ser Ile Leu Val Gly Cys Gly Lys
            20                  25                  30
Lys Glu Lys His Ser Val Thr Glu Ile Ala Unk Glu Lys Lys Arg Ile
        35                  40                  45
```

```
Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp Ser Val Lys Gln
    50                  55                  60

Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val Gly Gln Met Leu
65                  70                  75                  80

Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met Ser Gln Tyr Thr
                85                  90                  95

Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala Ala Leu Asn Leu
            100                 105                 110

Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His Leu Gly Thr Asp
        115                 120                 125

Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp Tyr His Tyr Lys
    130                 135                 140

Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln Asn Arg Pro Ala
145                 150                 155                 160

Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly Asn Ile Asn Leu
                165                 170                 175

Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe Leu Lys Ala Leu
            180                 185                 190

Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln Ala Ile Asn Tyr
        195                 200                 205

Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu Tyr Asp Lys Ala
    210                 215                 220

Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Asn Met Ala Glu Asn
225                 230                 235                 240

Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly Glu Val Asp Glu
                245                 250                 255

Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr Ala Thr Ala Tyr
            260                 265                 270

Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp Leu Asn Ser Cys
        275                 280                 285

Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn Glu Arg Leu Tyr
    290                 295                 300

Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys Glu Ile Asn Ser
305                 310                 315                 320

Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr Glu Asn Leu Glu
                325                 330                 335
```

```
Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe Cys Leu Ser Lys
            340                 345                 350
Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val Ser Ser Ile Gln
        355                 360                 365
Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln Lys Glu Leu Glu
    370                 375                 380
Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys Ser Lys Phe Ile
385                 390                 395                 400
Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile Leu Leu Ile Ser
                405                 410                 415
Val Leu Thr Tyr Ala Tyr Arg Gln Gly Lys Lys His Asn Lys Leu Ile
            420                 425                 430
Lys Glu Thr Asp Lys Leu Arg Ser Gly Phe Phe Thr Gly Ile Thr His
        435                 440                 445
Glu Phe Arg Thr Pro Ile Thr Val Ile Gln Gly Leu Asn Glu Lys Met
    450                 455                 460
Ser Ser Ser Pro Asp Leu Gln Ala Ser Asp Arg Thr Glu Leu His Lys
465                 470                 475                 480
Ile Ile Asp Arg Gln Ser Ser His Met Leu Asn Leu Val Asn Gln Leu
                485                 490                 495
Leu Asp Ile Cys Lys Ile Arg Ser Gly Val Ser Thr Pro Glu Trp Arg
            500                 505                 510
Asn Gly Asp Ile Val Ser Phe Val Gln Ile Leu Ile Asp Ser Phe Ala
        515                 520                 525
Pro Tyr Ala Gln Ala Gln Asp Ile Thr Leu Glu Leu Gln Pro Glu Ser
    530                 535                 540
Lys Pro Ile Val Val Asp Phe Val Pro Ser Tyr Leu Gln Lys Ile Ile
545                 550                 555                 560
Ser Asn Leu Leu Ser Asn Ala Ile Lys Tyr Ser Leu Ala Gly Gly Arg
                565                 570                 575
Val Val Ile Ser Leu Ala Lys Thr Lys Asn Glu Lys Asn Leu Ile Ile
            580                 585                 590
Arg Val Ala Asp Asn Gly Ile Gly Ile Asp Lys Thr Asp Gln Ala His
        595                 600                 605
Ile Phe Asp Ile Phe Tyr Arg Gly Gln Ser Ala Thr Glu Lys His Gly
    610                 615                 620
```

```
Ser Gly Val Gly Leu Ser Phe Thr Asn Ile Leu Val Glu Asn Leu Arg
625                 630                 635                 640
Gly Thr Ile Lys Val Glu Ser Gln Pro Gly Lys Gly Ser Ala Phe Thr
                645                 650                 655
Ile Ser Ile Pro Thr Gln Asn Gln Ser Ser Ser Ala Glu Ile Leu Pro
            660                 665                 670
Trp Leu Pro Ser Ser Asp Asp Ile Val Met Pro Val His Ile Ala Pro
        675                 680                 685
Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu Asn His Arg Phe
    690                 695                 700
Glu Asp Glu Arg Pro Thr Ile Leu Leu Val Glu Asp Asn Lys Asp Ile
705                 710                 715                 720
Asn Leu Leu Val Lys Leu Leu Leu Cys Asp Arg Tyr Asn Val Leu Ser
                725                 730                 735
Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr Glu His Ile Pro
            740                 745                 750
Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met Asp Gly Ile Glu
        755                 760                 765
Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys His Ile Pro Ile
    770                 775                 780
Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg Leu Glu Gly Ile
785                 790                 795                 800
Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe Ser Pro Glu Glu
                805                 810                 815
Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg Glu Leu Leu Lys
            820                 825                 830
Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys Pro Glu Glu Glu
        835                 840                 845
Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu Leu Ala Ala Lys
    850                 855                 860
Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp Phe Ser Ala Gln
865                 870                 875                 880
Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln Leu Asn Arg Lys
                885                 890                 895
Leu Thr Ser Val Val Gly Cys Ser Thr Ile Gly Tyr Ile Gln Gln Ile
            900                 905                 910
```

```
Lys Ile Lys Leu Ala Cys Lys Leu Leu Ala Asp Glu Ser Lys Asn Ile
        915                 920                 925
Ser Asp Ile Ser Ile Glu Ala Gly Phe Ser Asp Pro Ala Tyr Phe Ser
    930                 935                 940
Arg Thr Phe Lys Arg Tyr Met Asn Cys Ser Pro Ser Gln Tyr Arg Gln
945                 950                 955                 960
Lys Leu Leu Ala Met Pro Gly Ser Asp Lys Glu Thr Val
                965                 970
```

(2) INFORMATION FOR SEQ ID NO:59

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59

```
Tyr Lys Gln Ala Ile Met Lys His Leu Phe Lys Ser Thr Leu Val Leu
1               5                   10                  15
Leu Cys Ala Leu Ser Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn
            20                  25                  30
Asn Thr Glu Lys Ser Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly
        35                  40                  45
Tyr Ile Ala Gly Ser Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala
```

```
    50                  55                  60
Asn Asp Arg Leu Leu Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser
65                  70                  75                  80
Lys Lys Glu Asn Ala Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser
                85                  90                  95
Pro Gly Tyr Tyr Val Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr
            100                 105                 110
Ala Phe Tyr Val Val Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg
        115                 120                 125
Pro Ile Lys Asn Phe Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala
    130                 135                 140
Trp Met Ser Arg His Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp
145                 150                 155                 160
Asp Lys Gln Arg Lys Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met
                165                 170                 175
His Leu Gln Unk His Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr
            180                 185                 190
Asp Leu Thr Ser Cys Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln
        195                 200                 205
Lys Asp Arg Thr Phe Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly
    210                 215                 220
Leu Asn Leu
225
```

(2) INFORMATION FOR SEQ ID NO:60

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60

```
Met Lys Thr Ile Ser Lys Asn His Ala Ala Arg Ile Cys Ala Ala Ile
1               5                   10                  15
Ala Leu Phe Ala Val Cys Asn Gly Arg Ile Ala Ala Gln Asp Phe Leu
            20                  25                  30
Tyr Glu Ile Gly Gly Gly Phe Gly Ala Ala Gln Tyr Phe Gly Asp Ala
        35                  40                  45
Asn Arg Gly Leu Phe Gly Ser Ser Gly Val Gly Leu Glu Leu Val Gly
    50                  55                  60
Arg Tyr Asn Tyr Asn Phe Arg Trp Ala Phe Ser Thr Met Leu Asp Trp
65                  70                  75                  80
Arg Thr Leu Arg Gly Asp Thr Asp Lys Ser Gly Asn Val Phe Pro Asp
                85                  90                  95
Phe Ala Gln Ala Asp Phe Lys Val Gly Leu Thr Gln Leu His Val Arg
            100                 105                 110
Ser Glu Phe Asn Phe Leu Pro Tyr Ser Asp Gly Tyr Lys Tyr Leu Gly
        115                 120                 125
Thr Ala Arg Leu Ser Pro Tyr Val Ala Ala Gly Leu Ser Leu Gly Phe
    130                 135                 140
Ala Ser Gly Ala Lys Gly Ser Ala Phe Ala Pro Gly Ile Thr Ala Gly
145                 150                 155                 160
Met Gly Val Lys Tyr Lys Leu Lys Pro Arg Ile Asn Val Gly Ile Glu
                165                 170                 175
Tyr Ser Phe Thr Gly Leu Leu Thr Asp Ala Leu Asp Ala Leu Thr Asp
            180                 185                 190
Lys Ser Val Trp Leu Glu Asp Pro Tyr Lys Ile Asn Asp Ser Trp Val
        195                 200                 205
Lys Asn Lys Asp Ala Thr Gly Ala Leu Val Leu Arg Ile Thr Tyr Asp
    210                 215                 220
```

```
Phe Gly Leu Arg Lys Thr Phe Cys Asn Lys Gln
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:61

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1162 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

```
Ala Ile Ser Gln Met Lys Arg Ile Leu Pro Ile Val Ala Phe Leu Ser
1               5                   10                  15
Leu Phe Leu Ala Leu Ala Leu Pro Ala Lys Ala Gln Arg Ala Met Gly
            20                  25                  30
Lys Thr Ala Asp Arg Ser Leu Met Ala Ser Gly His Trp Val Lys Ile
        35                  40                  45
Arg Val Asp Ala Ser Gly Val Tyr Arg Leu Thr Asp Glu Gln Leu Arg
    50                  55                  60
Ala Asn Gly Phe Ser Asp Pro Ser Lys Val Gly Val Phe Gly Tyr Gly
65                  70                  75                  80
Gly Gly Val Leu Pro Glu Asp Leu Ser Arg Ile Thr Thr Asp Asp Leu
                85                  90                  95
Pro Pro Val Pro Val Leu Arg Gln Gly Asn Ala Leu Tyr Phe Tyr Ala
```

100 105 110

Val Gly Pro Val Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu

115 120 125

His Thr Val Asn Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp

130 135 140

Ala Ala Gly Ala Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala

145 150 155 160

Ser Ala Glu Ala Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu

165 170 175

Gln Glu Leu Tyr Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu

180 185 190

Ser Phe Ser Ala Val Asn Thr Arg Thr Val Lys Phe Pro Leu Arg Gly

195 200 205

Asn Thr Arg Ser Ser Gly Glu Leu Gly Thr Val Phe Ser Tyr Ile Ala

210 215 220

Lys Ala Arg Ser Ala Gly Gly Gly Arg Glu Met Ser Leu Ser Ala Asn

225 230 235 240

Gly Ile Leu Ile Phe Ser Asp Pro Phe Ser Met Thr Ser Asn Glu Val

245 250 255

Ser Asn Ser Tyr Leu Ala Gly Lys Lys Arg Arg Leu Tyr His Ser Thr

260 265 270

Pro Met Asn Ser Leu Val Asn Glu Leu Arg Leu Asp Ala Asn Tyr Ser

275 280 285

Met Thr Gly Asp Ala Val Asn Leu Asp Phe Ile Glu Val Ala Thr Gln

290 295 300

Asn Asp Leu Arg Tyr Asp Gly Ala Pro Met His Ile Arg Arg Phe Ser

305 310 315 320

Asn Leu Pro Val Leu Gly Gly Glu Ser Cys Arg Phe Val Ile Ser Glu

325 330 335

Val Pro Glu Ser Leu Val Val Leu Gln Ala Asn Ser Ser Leu Thr Ala

340 345 350

Ser Leu Val Pro Val Lys Thr Val Gly Asp Lys Thr Ile Glu Phe Val

355 360 365

Ala Pro Pro Lys Gly Gln Asp Arg Arg Thr Ile Asn Thr Phe Tyr Ala

370 375 380

Val Asp Leu Ser Gln Ala Ser Ala Pro Glu Ile Leu Gly Ala Val Pro

```
385                 390                 395                 400
Asn Gln Asn Leu His Gly Glu Glu Ile Pro Asp Leu Ile Ile Val Ser
                405                 410                 415
Thr Gln Ala Leu Leu Leu Glu Ala Asp Arg Leu Ala Thr Tyr Arg Arg
            420                 425                 430
Glu Lys Asn Gly Leu Lys Val Leu Val Val Leu Gln Glu Gln Val Phe
        435                 440                 445
Asn Glu Phe Ser Gly Gly Thr Pro Asp Ala Thr Ala Tyr Arg Leu Phe
    450                 455                 460
Ala Lys Met Phe Tyr Asp Arg Trp Lys Ala Asn Ala Pro Val Gly Glu
465                 470                 475                 480
Thr Phe Pro Met Gln Met Leu Leu Phe Gly Asp Gly Ala His Asp Asn
                485                 490                 495
Arg Lys Val Ser Val Ala Trp Gln Lys Pro Tyr Leu Gln Gln Thr Glu
            500                 505                 510
Phe Leu Leu Thr Phe Gln Ala Val Asn Ser Thr Asn Val Asn Ser Tyr
        515                 520                 525
Val Thr Asp Asp Tyr Phe Gly Leu Leu Asp Asp Gln Pro Ala Ser Val
    530                 535                 540
Asn Ile Gly Trp Arg Asn Tyr Asn Met Ala Val Gly Arg Phe Pro Val
545                 550                 555                 560
Arg Thr Pro Ala Glu Ala Arg Ile Ala Val Asp Lys Thr Ile Arg Tyr
                565                 570                 575
Glu Glu Asp Arg Glu Ser Gly Ala Trp Arg Ile Arg Ala Cys Phe Ala
            580                 585                 590
Ala Asp Asn Gly Asp Lys His Ala Thr Glu Thr Ser Arg Leu Ile Asp
        595                 600                 605
Thr Val Lys Arg Tyr Ala Pro Ala Ile Met Pro Val Arg Ala Phe Gln
    610                 615                 620
Asp Val Tyr Pro His Val Ile Glu Asn Gly Leu His Ser Ile Pro Gly
625                 630                 635                 640
Ala Lys Lys Lys Met Leu Glu Thr Leu Gln Ser Gly Ile Ile Leu Leu
                645                 650                 655
Asn Tyr Ala Gly His Gly Gly Pro Ala Gly Trp Ser Asp Glu His Leu
            660                 665                 670
Leu Thr Leu Asn Asp Ile His Lys Phe Asn Tyr Lys His Met Pro Ile
```

```
        675                 680                 685
Trp Ile Thr Ala Thr Cys Asp Phe Ala Asn Tyr Asp Ser Gln Thr Thr
    690                 695                 700
Ser Ala Gly Glu Glu Val Phe Leu His Glu Lys Ser Gly Thr Pro Ile
705                 710                 715                 720
Met Phe Ser Thr Thr Arg Val Val Tyr Asn Thr Gln Asn Glu Lys Ile
                725                 730                 735
Asn Gly Phe Met Leu Arg Arg Met Phe Glu Lys Ala Lys Asp Gly Arg
            740                 745                 750
Tyr Arg Thr Met Gly Glu Ile Ile Arg Ser Ala Lys Gln Gly Met Leu
        755                 760                 765
Ser Thr Val Phe Pro Asp Ser Ile Asn Gln Leu Ser Phe Phe Leu Met
    770                 775                 780
Gly Asp Pro Ser Val Arg Met Asn Leu Pro Thr His Lys Val Gln Leu
785                 790                 795                 800
Thr Ala Ile Asn Gly Gln Asp Pro Glu Gly Gln Tyr Gly Thr Ile Met
                805                 810                 815
Leu Lys Ser Leu Glu Arg Val Ala Leu Lys Gly Lys Val Thr Asp Glu
            820                 825                 830
Lys Gly Thr Phe Asp Glu Thr Phe Ser Gly Lys Val Phe Leu Thr Val
        835                 840                 845
Phe Asp Gly Arg Lys Lys Met Thr Ala Leu Glu Glu Glu Gly Asn Asp
    850                 855                 860
Leu Ser Leu Val Tyr Tyr Asp Tyr Pro Asn Val Met Tyr Ala Gly Ile
865                 870                 875                 880
Ala Glu Val Lys Asp Gly Leu Phe Glu Thr Ser Phe Ile Val Pro Lys
                885                 890                 895
Asp Val Asn Tyr Ser Glu His Glu Gly Arg Ile Asn Leu Tyr Ala Tyr
            900                 905                 910
Asn Glu Ser Thr Lys Ala Glu Ala Met Gly Val Asp Phe Ser Ile Arg
        915                 920                 925
Val Gln Pro Gly Ile Pro Asp Glu Val Thr Glu Asp Asn Thr Pro Pro
    930                 935                 940
Glu Ile Ile Ser Cys Phe Leu Asn Asp Ser Thr Phe Arg Ser Gly Asp
945                 950                 955                 960
Glu Val Asn Pro Thr Pro Leu Phe Met Ala Glu Val Phe Asp Leu Asn
```

```
                    965                      970                      975
Gly Ile Asn Ile Thr Gly Ser Gly Val Gly His Asp Ile Thr Leu Cys
                980                      985                      990
Ile Asp Gly Arg Ala Asp Leu Thr Tyr Asn Leu Asn Ala Tyr Phe Thr
            995                     1000                     1005
Ser Ser Ala Thr Asp Ala Gly Val Gly Thr Ile Leu Phe Met Ile Pro
    1010                     1015                     1020
Ala Leu Ala Glu Gly Asp His Thr Ala Arg Leu Thr Val Trp Asp Ile
1025                    1030                     1035                    1040
Phe Asn Asn Ala Val His His Asp Phe Ser Phe Arg Val Val Asp Gly
                1045                     1050                     1055
Ile Ala Pro Asp Val Ala Asp Val Ile Leu Phe Pro Asn Pro Val Arg
            1060                     1065                     1070
Glu Ser Ala Thr Phe Arg Ile Phe His Asn Arg Pro Gly Ser Asp Leu
        1075                     1080                     1085
Asn Val Ala Val Glu Ile Tyr Asp Phe Thr Gly Arg Leu Val Asn Ser
    1090                     1095                     1100
Leu Pro Val Lys Thr Tyr Ser Ser Ser Tyr Gly Glu Pro Ile Glu Ile
1105                    1110                     1115                    1120
Lys Trp Asp Leu Thr Ser Lys Tyr Gly Val Lys Ile Gly Asn Gly Phe
                1125                     1130                     1135
Tyr Leu Tyr Arg Cys Val Val Asn Ser Pro Gly Gly Gln Thr Ala Ser
            1140                     1145                     1150
Met Ala Lys Lys Met Ile Val Val Gly Gln
        1155                     1160
```

(2) INFORMATION FOR SEQ ID NO:62

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62

```
Ile Phe Ile Asp Pro Asp Lys Asn Thr Lys Gln Asn Glu Arg Asn Met
1               5                   10                  15
Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile Leu
            20                  25                  30
Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn Val
        35                  40                  45
Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg Ala
    50                  55                  60
Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr Ser
65                  70                  75                  80
Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala Gly
                85                  90                  95
Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp Ile
            100                 105                 110
Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu Asn
        115                 120                 125
Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu Glu
    130                 135                 140
Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn Glu
145                 150                 155                 160
Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe Ser
                165                 170                 175
Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His Asn
            180                 185                 190
Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala Gly
        195                 200                 205
```

```
Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp Ser
    210                 215                 220
Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp Gly
225                 230                 235                 240
Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr Gly
                245                 250                 255
Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu Glu
            260                 265                 270
Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn Asp
        275                 280                 285
Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser Ser
    290                 295                 300
Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu Lys
305                 310                 315                 320
Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser Tyr
                325                 330                 335
Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro Thr
            340                 345                 350
Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met Asn
        355                 360                 365
Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser Asn
    370                 375                 380
Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp Gly
385                 390                 395                 400
Leu Arg Asn Leu Phe His
                405
```

(2) INFORMATION FOR SEQ ID NO:63

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63

```
Thr Arg Glu Ser Val Leu His Cys Arg Thr Lys Leu Lys Lys Glu Arg
1               5                   10                  15
Lys Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile
            20                  25                  30
Gly Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn
        35                  40                  45
Phe Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn
    50                  55                  60
Asn Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala
65                  70                  75                  80
Leu Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met
                85                  90                  95
Arg Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His
            100                 105                 110
Tyr Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp
        115                 120                 125
Asn Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val
    130                 135                 140
Ala Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp
145                 150                 155                 160
Ala Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu
                165                 170                 175
Ser Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu
            180                 185                 190
His Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu
```

195 200 205

Arg Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe

210 215 220

(2) INFORMATION FOR SEQ ID NO:64

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64

Lys Gly Thr Trp Asn Arg Lys Asn Arg Arg Glu Glu Met Lys Arg Thr

1 5 10 15

Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu Ser Leu Leu Arg

20 25 30

Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met Ser Gly Leu Ser

35 40 45

Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn Leu Asn Leu Arg

50 55 60

Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser Leu Asp Ala Ala

65 70 75 80

Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile Gly His Asn Tyr

85 90 95

```
Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr Val Asp Arg Ser
            100                 105                 110
Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val Glu Val Phe Ser
        115                 120                 125
Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys Tyr Asn Val Glu
    130                 135                 140
Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp Leu Ser Leu Gln
145                 150                 155                 160
Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln Glu Met Thr Arg
                165                 170                 175
Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln Arg Asn Arg Thr
            180                 185                 190
Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly Lys Leu Leu Asp
        195                 200                 205
Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu Val Gln Tyr Arg
    210                 215                 220
Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln Ala Leu Glu Leu
225                 230                 235                 240
Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp Thr Asp Val Leu
                245                 250                 255
Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu Glu Ile Tyr Arg
            260                 265                 270
Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser Glu Leu Gln Ile
        275                 280                 285
Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala Ala Tyr Phe Pro
    290                 295                 300
Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr Phe Arg Asp Leu
305                 310                 315                 320
Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser Glu Gln Trp Lys
                325                 330                 335
Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn Ile Pro Ile Phe
            340                 345                 350
Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser Arg Leu Gln Ile
        355                 360                 365
Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys Ala Leu Tyr Lys
    370                 375                 380
```

Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala Asp Lys Ala Ile
385 390 395 400
Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys Ala Tyr Glu Tyr
405 410 415
Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala Tyr Glu Tyr Ala
420 425 430
Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu Glu Leu Arg Ala
435 440 445
Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp Phe Tyr Gln Gly
450 455 460
Lys Asp Phe
465

(2) INFORMATION FOR SEQ ID NO:65

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 436 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65

Asn Ile Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp
1 5 10 15
Tyr Ala Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala

```
            20                  25                  30
Gln Asn Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly
        35                  40                  45
Arg Leu Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu
    50                  55                  60
Gly Val Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala
65                  70                  75                  80
Ser Tyr Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala
                85                  90                  95
Ser Thr Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg
            100                 105                 110
Lys Met Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys
        115                 120                 125
Ser Ile Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr
    130                 135                 140
Gln Phe Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr
145                 150                 155                 160
Arg Lys Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile
                165                 170                 175
Gly Ala Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser
            180                 185                 190
Leu Phe Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu
        195                 200                 205
Ala Pro Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala
    210                 215                 220
Lys Phe Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg
225                 230                 235                 240
Ser Leu Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser
                245                 250                 255
Glu Leu Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu
            260                 265                 270
Ser Glu Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro
        275                 280                 285
His Thr Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu
    290                 295                 300
Leu Gly Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr
```

```
305                 310                 315                 320
Lys Ser Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly
                325                 330                 335
Glu Ile Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg
            340                 345                 350
Tyr Arg Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr
        355                 360                 365
Lys Gly Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly
    370                 375                 380
Ile Gly Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu
385                 390                 395                 400
Glu Tyr Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala
                405                 410                 415
Leu Lys Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys
            420                 425                 430
Leu Lys Leu Asn
        435
```

(2) INFORMATION FOR SEQ ID NO:66

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66

```
Asn Thr Ile Ser Glu Asn Gly Asn Asp Ser Thr Tyr Phe Ser Phe Gln
1               5                   10                  15
Thr Phe Leu Met Arg Ser Ile Tyr Gln Leu Leu Leu Ser Ile Leu Leu
            20                  25                  30
Ala Ser Leu Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala
        35                  40                  45
Gly Arg Val Leu Asp Glu Glu Gly Asn Pro Met Ile Gln Ala Asn Val
    50                  55                  60
Gln Leu Val Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr
65                  70                  75                  80
Asn Glu Lys Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr
                85                  90                  95
Ile Leu Arg Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile
            100                 105                 110
Ser Leu Arg Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn
        115                 120                 125
Glu Asp Ala Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala
    130                 135                 140
Glu Val Val Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr
145                 150                 155                 160
Thr Val Ala Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro
                165                 170                 175
Gly Ala Glu Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp
            180                 185                 190
Ile Ser Lys Ile Leu Val Asp Gly Lys Glu Phe Phe Ser Lys Asp Pro
        195                 200                 205
Gln Val Ala Ile Lys Asn Leu Pro Ala Asp Met Val Asn Lys Val Gln
    210                 215                 220
Val Leu Asn Lys Leu Ser Glu Leu Ser Arg Met Ser Gly Phe Asp Asp
225                 230                 235                 240
Gly Glu Glu Glu Thr Val Ile Asn Leu Thr Val Lys Pro Glu Lys Lys
                245                 250                 255
Lys Gly Leu Phe Gly Thr Leu Gln Ala Gly Tyr Gly Thr Asp Gln Arg
            260                 265                 270
```

```
Tyr Met Ala Gly Gly Asn Val Asn Arg Phe Asp Gly Asn Lys Gln Trp
        275                 280                 285
Thr Leu Ile Gly Ser Ala Asn Asn Thr Asn Asn Met Gly Phe Ser Glu
    290                 295                 300
Met Asp Ser Glu Met Gly Ser Met Thr Phe Phe Ser Pro Gln Gly Gly
305                 310                 315                 320
Gly Arg Arg Gly Phe Gly Asn Ser Gly Gly Val Thr Ser Ser Ser Met
                325                 330                 335
Leu Gly Gly Asn Phe Ser Val Glu Phe Ser Ser Ala Leu Asn Thr Gly
            340                 345                 350
Gly Asp Ala Arg Tyr Gly Tyr Asn Asp Lys Ala Ile Glu Thr Thr Lys
        355                 360                 365
Arg Val Glu Asn Ile Leu Ala Glu Gly Asn Thr Tyr Met Asp Glu Asn
    370                 375                 380
Ile Leu Glu Arg Ser Phe Ser His Asn Gly Gln Ala Arg Phe Arg Met
385                 390                 395                 400
Gln Trp Lys Pro Ser Glu Arg Thr Glu Val Val Phe Glu Pro Asp Leu
                405                 410                 415
Ser Ile Ser Lys Ile Asp Gly Phe Phe Asn Asp Thr Tyr Glu Thr Lys
            420                 425                 430
Asp Ala Thr Gly Ile Ser Ile Asn Lys Gly Ser Ile His Gln Thr Thr
        435                 440                 445
Gln Gly Asn Asn Phe Arg Leu Asn Gly Glu Leu Asp Ile Ser His Lys
    450                 455                 460
Leu Asn Asp Glu Gly Arg Thr Ile Ser Ala Ser Val Ser Gly Gly Leu
465                 470                 475                 480
Thr Asp Glu Asp Gly Asp Gly Ile Tyr Gln Ala Val Leu Gln Ser Val
                485                 490                 495
Glu Thr Asn Gln Lys Gln Phe Asn Asp Asn Ser Asn Leu Gln Tyr Arg
            500                 505                 510
Leu Arg Leu Ser Tyr Val Glu Pro Leu Gly Lys Asn Tyr Phe Ala Gln
        515                 520                 525
Ala Ile Leu Asn Arg Arg Phe Ser Arg Arg Asn Ser Asp Arg Glu Val
    530                 535                 540
Tyr Arg Leu Gly Asp Asp Gly Gln Tyr Ser Ile Leu Asp Ser Gln Tyr
545                 550                 555                 560
```

```
Gly Leu Ser Tyr Ser Asn Glu Phe Thr Gln Tyr Arg Ile Gly Leu Asn
                565                 570                 575
Leu Lys Lys Ile Ala Lys Thr Trp Asp Tyr Thr Val Gly Phe Asn Val
            580                 585                 590
Asp Pro Asn Arg Thr Val Ser Tyr Arg Ser Val Ala Gly Val Glu Gln
        595                 600                 605
Asp Lys Leu Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile
    610                 615                 620
Asn Tyr Lys Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly
625                 630                 635                 640
Arg Thr Thr Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile
                645                 650                 655
Thr Asn Pro Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser
            660                 665                 670
Tyr Ser Asn Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser
        675                 680                 685
Gln Arg Ala Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp
    690                 695                 700
Ile Val Pro Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr
705                 710                 715                 720
Arg Tyr Glu Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr
                725                 730                 735
Leu Ser Leu Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu
            740                 745                 750
Phe Asn Arg Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn
        755                 760                 765
Lys Ala Leu Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg
    770                 775                 780
Asn Asn Trp Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met
785                 790                 795                 800
Ala Asn Asn Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe
                805                 810                 815
Gly Gly Asn Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile
            820                 825                 830
Asp Ser Asp Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe
        835                 840                 845
```

Ser Leu Asp Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu
850 855 860
Arg Asp Lys Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly
865 870 875 880
Gln Arg Ser Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu
885 890 895
Ser Met Ser Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr
900 905 910
Arg Phe Asn Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg
915 920 925
Gly Asn Met Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro
930 935 940
Ser
945

(2) INFORMATION FOR SEQ ID NO:67

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 790 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...790

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67

Leu Leu Phe Ser Ser Pro Leu Pro Arg Met Asp Arg Pro Lys Pro Ser

1 5 10 15
Tyr Ile Val Arg Ile Ala Ala Ile Leu Cys Leu Phe Val Gly Arg Pro
20 25 30
Leu Phe Ala Gln Ser Tyr Val Asp Tyr Val Asp Pro Leu Ile Gly Thr
35 40 45
Leu Ser Ser Phe Glu Leu Ser Ala Gly Asn Thr Tyr Pro Val Ile Gly
50 55 60
Leu Pro Trp Gly Met Asn Ser Trp Thr Pro Met Thr Gly Val Pro Gly
65 70 75 80
Asp Gly Trp Gln Tyr Thr Tyr Ser Ala His Lys Ile Arg Gly Phe Lys
85 90 95
Gln Thr His Gln Pro Ser Pro Trp Ile Asn Asp Tyr Gly Gln Phe Ser
100 105 110
Leu Leu Pro Leu Thr Ala Pro Gln Lys Pro Ser Ser Asn Asp Ser Ile
115 120 125
Ala Leu Thr Lys Trp Cys Lys Gln Leu Phe Ser Asp Glu Gln Thr Ser
130 135 140
Trp Phe Ser His Lys Ala Glu Thr Ala Thr Pro Tyr Tyr Tyr Ser Val
145 150 155 160
Tyr Leu Ala Asp Tyr Asp Thr Arg Val Glu Met Ala Pro Thr Glu Arg
165 170 175
Ala Ala Ile Phe Arg Ile Arg Tyr Ser Gly Asn Thr Glu Ser Gly Ser
180 185 190
Gly Arg Trp Leu Arg Leu Asp Ala Phe Thr Gly Gly Ser Glu Ile Ser
195 200 205
Ile Val Asp Pro His Thr Val Val Gly Ile Ser Arg Lys Asn Ser Gly
210 215 220
Gly Val Pro Ala Asn Phe Ala Cys Tyr Phe Ile Leu Gln Ser Asp Thr
225 230 235 240
Pro Met Ala Asp Val Leu Leu Glu Thr Asp Thr Gly Lys Ser Asp Glu
245 250 255
Gly Thr Arg Ala Trp Ala Ala Cys Arg Phe Asp Ser Gln Glu Val Thr
260 265 270
Val Arg Val Ala Ser Ser Phe Ile Ser Val Glu Gln Ala Glu Arg Asn
275 280 285
Leu Ala Glu Val Lys Gly Gln Ser Phe Asp Arg Ile Arg Leu Ala Gly

290 295 300
Arg Glu Ala Trp Asn Lys Val Leu Gly Arg Ile His Val Glu Gly Gly
305 310 315 320
Thr Lys Asp Glu Arg Thr Thr Phe Tyr Ser Ala Leu Tyr Arg Cys Leu
325 330 335
Leu Phe Pro Arg Arg Phe Tyr Glu Glu Asp Ala Ser Gly Asn Phe Val
340 345 350
His Tyr Ser Pro Tyr Asn Gly Glu Val Leu Pro Gly Tyr Leu Tyr Thr
355 360 365
Asp Thr Gly Phe Trp Asp Thr Phe Arg Ala Leu Phe Pro Leu Leu Asn
370 375 380
Leu Leu Tyr Pro Asp Glu Asn Ile Lys Ile Gln Glu Gly Leu Leu Asn
385 390 395 400
Val Tyr Arg Glu Ser Gly Phe Phe Pro Glu Trp Ala Ser Pro Gly His
405 410 415
Arg Asp Cys Met Ile Gly Asn Asn Ser Ala Ser Val Leu Ala Asp Ala
420 425 430
Tyr Leu Lys Gly Val Arg Val Glu Asp Thr Arg Thr Leu Met Asn Gly
435 440 445
Leu Leu His Ala Thr Lys Ala Val His Pro Lys Ile Ser Ser Thr Gly
450 455 460
Arg Lys Gly Trp Glu Trp Tyr Asn Ser Leu Gly Tyr Val Pro Ala Asp
465 470 475 480
Ala Gly Ile Asp Glu Ser Ala Ala Arg Thr Leu Glu Tyr Ala Tyr Asn
485 490 495
Asp Trp Cys Ile Leu Arg Leu Gly Arg Thr Leu Gly Trp Asp Arg Ala
500 505 510
Ala Leu Asp Thr Leu Ala His Arg Ser Met Asn Tyr Arg His Leu Phe
515 520 525
Asp Pro Glu Thr Lys Leu Met Arg Gly Arg Asn Gln Asp Gly Ser Phe
530 535 540
Arg Thr Pro Phe Ser Pro Phe Lys Trp Gly Asp Val Phe Thr Glu Gly
545 550 555 560
Asn Ala Trp His Tyr Thr Trp Ser Val Phe His Asp Val Gln Gly Leu
565 570 575
Ile Asp Leu Met Gly Gly Asp Arg Pro Phe Val Ser Met Leu Asp Ser

```
            580                 585                 590
Val Phe Asn Thr Pro Pro Met Phe Asp Glu Ser Tyr Tyr Gly Phe Val
        595                 600                 605
Ile His Glu Ile Arg Glu Met Gln Ile Ala Asp Met Gly Asn Tyr Ala
    610                 615                 620
His Gly Asn Gln Pro Ile Gln His Met Ile Tyr Leu Tyr Asn His Ala
625                 630                 635                 640
Gly His Pro Trp Lys Ala Gln Glu Arg Leu Arg Glu Val Met Gly Arg
                645                 650                 655
Leu Tyr Arg Pro Thr Pro Asp Gly Tyr Cys Gly Asp Glu Asp Asn Gly
            660                 665                 670
Gln Thr Ser Ala Trp Tyr Val Phe Ser Ala Leu Gly Phe Tyr Pro Val
        675                 680                 685
Thr Pro Ala Thr Asp Gln Tyr Val Leu Gly Ser Pro Ile Phe Ser Lys
    690                 695                 700
Val Ile Leu Ser Phe Pro Asp Gly His Lys Thr Val Leu His Ala Pro
705                 710                 715                 720
Ala Asn Ser Ala Asp Thr Pro Tyr Ile Arg Ser Ile Ser Val Glu Gly
                725                 730                 735
Lys Glu Trp Ser Cys Asn Tyr Leu Thr His Glu Gln Leu Arg Ser Ser
            740                 745                 750
Ala Ser Ile Gln Trp Met Met Asp Thr Lys Pro Asn Tyr Asn Arg Gly
        755                 760                 765
Met Lys Glu Ser Asp Arg Pro Tyr Ser Phe Ser Thr Glu Gln Gln Arg
    770                 775                 780
Arg Ala Asn His Ser Asn
785                 790
```

(2) INFORMATION FOR SEQ ID NO:68

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68

```
Leu Ile Ile Glu Lys Glu Met Lys Thr Thr Val Gln Gln Ile Ile Leu
1               5                   10                  15
Cys Leu Ala Leu Met Met Ser Gly Val Leu Gly Gly Asn Ala Gln Ser
            20                  25                  30
Phe Trp Glu Glu Ile Ala Pro Pro Phe Ile Ser Asn Glu Pro Asn Val
        35                  40                  45
Lys Tyr Ile Ile Pro Asn Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr
    50                  55                  60
Val Thr Val Thr Lys Arg Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu
65                  70                  75                  80
Gln Leu Gly Met Tyr Tyr Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp
                85                  90                  95
Lys His Asp Pro Tyr Phe Asp Asp Lys Ile Val Ala Asp Ile Gln Thr
            100                 105                 110
Asp Ala Tyr Gly Arg Val Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln
        115                 120                 125
Glu Tyr Gln Leu Tyr Ile Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe
    130                 135                 140
Lys Thr Ser Val Ser Thr Tyr Glu His Gly Met Ala Val Phe Arg Ser
145                 150                 155                 160
Ser Thr Gly Val Thr Tyr Ile Gly Thr Arg His His Ile Phe Ala Ser
                165                 170                 175
Gly Val Asn Asp Phe Glu Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro
            180                 185                 190
```

```
Met Ser Cys Arg Phe Ala Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu
        195                 200                 205
Ala Leu Met His Glu Thr Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln
    210                 215                 220
Asn Gly Glu Phe Val Asp Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile
225                 230                 235                 240
Ile Ala Ser Met Cys Ser Asn Lys Glu Gly Asp Ile Ile Ala Leu Val
                245                 250                 255
Thr Ser Tyr Thr Gly Phe Met Ser Gly Thr Leu Ala Ile Arg Lys Ala
            260                 265                 270
Asp Glu Gly Lys Trp Gln Leu Val Gly Gly Asp Ile Gln Asn Ala Ile
        275                 280                 285
Val Gln Asn Ile Cys Met Met Asp Asp Asn Lys Ile Ala Cys Glu Val
    290                 295                 300
Phe Gly Thr Pro Asn Gly Val Asp Gly Arg Thr Arg Val Cys Val Ser
305                 310                 315                 320
Asp Ala Ser Val Phe Asp Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly
                325                 330                 335
Gly Leu Ile Phe Asp Thr Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu
            340                 345                 350
Tyr Ala Lys Phe Gly Gly Ile Met Leu Arg Ser Lys Glu Ser Phe Ile
        355                 360                 365
Thr Ser Phe Ile Ser Pro Thr Val Val Gln Gly Val Asp Val Tyr Thr
    370                 375                 380
Leu Ala Gly Lys Ile Arg Ile Glu Ser Glu Thr Pro Val Ser Glu Val
385                 390                 395                 400
Leu Leu Phe Asp Leu Ala Gly Arg Met Val Leu Arg Gln Thr Ile Asp
                405                 410                 415
Asn Lys Ile Tyr Ser Asp Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly
            420                 425                 430
Ile Tyr Val Val Ser Val Arg Leu Ser Ser Gly Gln Val Phe Ser His
        435                 440                 445
Lys Val Gln Val
    450
```

(2) INFORMATION FOR SEQ ID NO:69

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 331 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69

```
Gly Leu Tyr Gly Met Ser Val Val Pro Ile Ile Ile Tyr Leu Cys Gly
1               5                   10                  15
Ile Ser Asn Tyr Ala Arg Leu Met Ile Ile Arg Cys Leu Ile Arg Arg
            20                  25                  30
Pro Arg Thr Val Leu Phe Gly Leu Ile Phe Val Val Gly Leu Phe Ser
        35                  40                  45
Ala Met Ala Gln Glu Lys Lys Asp Ser Leu Ser Thr Val Gln Pro Val
    50                  55                  60
Pro Asn Ser Ser Met Val Glu Gln Thr Pro Leu Leu Ser Ile Asp His
65                  70                  75                  80
Pro Val Leu Pro Ala Ser Phe Gln Asn Thr Arg Thr Leu Lys Arg Phe
                85                  90                  95
Arg Asp Lys His Leu Ser Asp Ala Leu Leu Asn Gly Leu Lys Pro His
            100                 105                 110
Arg Ser Ser Leu Gln Leu Asn Glu Glu Leu Asn Phe Ala Ala Glu Arg
        115                 120                 125
Arg Asp Phe Val Ser Pro Leu Leu Gln Thr Arg His Ala Ala Gly Val
```

130 135 140

Leu Ser Trp Arg Pro Thr Asp Arg Met His Phe Tyr Thr Ser Gly Asn

145 150 155 160

Ile Gly Leu Gly His Asp Leu Leu Thr Gly Val Arg Lys Asp Phe Gly

165 170 175

Trp Asn Ala Gly Ala Asp Phe Leu Leu Ser Gln Asn Leu Thr Ala His

180 185 190

Val Gln Gly Gly Trp Gln Gln Asn Phe Gly Phe Ile Pro Met Thr Ala

195 200 205

Val Asn Gly Gln Leu Arg Trp Gln Ala Thr Glu Arg Leu Ser Phe Thr

210 215 220

Thr Gly Ile Asp Tyr Arg Gln Val Gln Trp Asn Ala Phe Asp Asn Arg

225 230 235 240

Thr Phe Ser Leu Lys Gly Ser Ala Arg Tyr Glu Val Met Asp Asn Val

245 250 255

Phe Val Asn Gly Phe Gly Ser Tyr Pro Leu Tyr Ser Ser Thr Arg Ser

260 265 270

Gly Leu Asn Met Ala Val Pro Met His Gly Phe Gly Pro Gln Tyr Gly

275 280 285

Gly Ser Leu Glu Leu Lys Val Ser Glu Arg Phe Gly Phe Ala Val Gly

290 295 300

Met Glu Arg Glu Tyr Asn Ile Trp Thr Arg Arg Trp Glu Thr His Tyr

305 310 315 320

Phe Ala Tyr Pro Val Phe Tyr Gly Asp Lys Lys

325 330

(2) INFORMATION FOR SEQ ID NO:70

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70

```
Ile Lys Arg Ile Glu Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu
1               5                   10                  15
Leu Ala Ser Val Thr Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg
            20                  25                  30
Val Asp Ala Asn Phe Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly
        35                  40                  45
Tyr Val Trp Asp Thr Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala
    50                  55                  60
Ala Glu Phe Met Ile Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu
65                  70                  75                  80
Asn Tyr Thr Met Lys Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met
                85                  90                  95
Val Pro Gly Thr Tyr Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu
            100                 105                 110
Gln Leu Pro Ile Asn Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met
        115                 120                 125
Ala Val Ser Ile Glu Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly
    130                 135                 140
Thr Tyr Arg Gln Lys Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr
145                 150                 155                 160
Glu Phe Phe Gly Pro Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp
                165                 170                 175
Ile Gly Ala Asn Ile Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile
            180                 185                 190
Gln Ile Gly Tyr Glu His Gly Phe Val Asp Ile Val Ser Gly Gly Gly
        195                 200                 205
```

```
Ser Asp Ile Pro Arg Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr
    210                 215                 220
Ala Leu Arg Glu Lys Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe
225                 230                 235                 240
Phe Val Gly Ile Gly Tyr Arg Phe
                245
```

(2) INFORMATION FOR SEQ ID NO:71

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 563 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71

```
Ser Leu Ile Asn Asn Ser Arg Asp Trp Arg Ala Pro Val Arg Leu Ser
1               5                   10                  15
Leu Lys Lys Lys Thr Lys Thr Met Lys Thr Lys Val Leu Arg Lys Phe
            20                  25                  30
Val Val Ala Ala Phe Ala Val Ala Thr Leu Cys Pro Leu Ala Gln Ala
        35                  40                  45
Gln Thr Met Gly Gly Asp Asp Val Lys Val Val Gln Tyr Asn Gln Glu
    50                  55                  60
Lys Leu Val Gln Thr Arg Met Ser Val Ala Asp Asn Gly Trp Ile Tyr
```

```
65                  70                  75                  80
Val Met Thr His Ser Gly Tyr Asp Thr Gly Asn Ser Asn Val Lys Ile
                85                  90                  95
Phe Arg Ser Lys Asp Gln Gly Ala Thr Tyr Gln Lys Leu Arg Asp Trp
            100                 105                 110
Asp Pro Ser Asp Asp Tyr Gln Phe Gln Asp Phe Asp Ile Val Val Thr
        115                 120                 125
Gly Lys Asn Glu Ser Asp Ile Lys Ile Trp Ser Val Glu Leu Met Asn
    130                 135                 140
Lys Pro Gly Gly Tyr Lys Ser Arg Val Ala Val Phe Ser Arg Asp Ala
145                 150                 155                 160
Asn Ala Gln Asn Ala Lys Leu Val Tyr Lys Glu Asp Phe Ser Asn Val
                165                 170                 175
Gln Leu Tyr Asp Val Asp Ile Ala Ser Asn Tyr Arg Ser Pro Ser Ser
            180                 185                 190
Leu Asn Asn Gly Gly Asn Pro Phe Ala Leu Ala Phe Ala Tyr Thr Gly
        195                 200                 205
Phe Asn Asn Thr His Lys Ile Ser Phe Val Asp Tyr Val Phe Ser Leu
    210                 215                 220
Asn Gly Gly Gln Asn Phe Asn Lys Asn Leu Leu Phe Ser Gln Asp Gly
225                 230                 235                 240
Glu Lys Lys Ile Asp Lys Val Asp Leu Ser Leu Gly Ser Thr Ser Glu
                245                 250                 255
Ser Met Gly His Asn Ala Trp Pro Leu Met Gly Val Val Phe Glu Met
            260                 265                 270
Asn Lys Gln Gly Gly Lys Ser Asp Ile Gly Phe Leu Ser Asn Phe Val
        275                 280                 285
Asp Asn Asp Pro Glu Phe Gln Trp Ser Gly Pro Ile Lys Val Ser Glu
    290                 295                 300
Ser Asp Met Ser Phe Ser Pro Lys Ile Gln Met Leu Leu Asp Glu Asp
305                 310                 315                 320
Asn Asn Thr Ile Asn Gly Glu Ser Cys His Asn Phe Met Ile Thr Tyr
                325                 330                 335
Ser Asp Tyr Asp Ser Glu Tyr Ser Asp Trp Asp Ile Arg Tyr Val Tyr
            340                 345                 350
Pro Lys Lys Ser Phe Lys Tyr Glu Lys Gly Lys Thr Pro Thr Met Asp
```

355 360 365

Asp Leu Val Glu Ala Phe Leu Thr Ala Ser Tyr Gln Ser Glu Thr Asn

370 375 380

Ser Gly Leu Gly Tyr Asp Lys Asn Ala Asn His Tyr Leu Ile Thr Tyr

385 390 395 400

Ala Lys Lys Glu Glu Asn Gly Thr Asn Thr Leu Lys Tyr Arg Trp Ala

405 410 415

Asn Tyr Asp Lys Ile His Asn Lys Asp Leu Trp Ser Asp Thr Phe Thr

420 425 430

Tyr Thr Ser Ser Ala Asn Ala Leu Tyr Thr Pro Gln Val Asp Ile Asn

435 440 445

Pro Thr Lys Gly Leu Val Cys Trp Ser Trp Val Glu Tyr Leu Pro Gly

450 455 460

Lys Arg Ile Val Trp Ser Asp Thr Gln Trp Thr His Ala Asn Gly Val

465 470 475 480

Glu Asp Ile Val Met Gln Glu Gly Ser Met Lys Leu Tyr Pro Asn Pro

485 490 495

Ala Gln Glu Tyr Ala Val Ile Ser Leu Pro Thr Ala Ala Asn Cys Lys

500 505 510

Ala Val Val Tyr Asp Met Gln Gly Arg Val Val Ala Glu Ala Ser Phe

515 520 525

Ser Gly Asn Glu Tyr Arg Leu Asn Val Gln His Leu Ala Lys Gly Thr

530 535 540

Tyr Ile Leu Lys Val Val Ser Asp Thr Glu Arg Phe Val Glu Lys Leu

545 550 555 560

Ile Val Glu

(2) INFORMATION FOR SEQ ID NO:72

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

```
Gly Ile Ile Ser Val Leu Ser His Val Val Asp Arg Pro Gln Trp Gly
1               5                   10                  15
Ala Ser Pro Glu Ala Ala Gly Thr His Ser Val Tyr Ser Ile Leu His
            20                  25                  30
Pro Ser Ala Gly Ile Ile Arg Ile Arg Ser Met Gly Ile Ile Ser Ala
        35                  40                  45
Cys Arg Ile Ala Ile Leu Ala Gly Lys His Pro Arg Ser Gly Leu Ser
    50                  55                  60
Arg Ala Asn Val Gly Ile Leu Ser Tyr Asn Pro Glu Asn Thr Pro Glu
65                  70                  75                  80
Lys Lys Arg Lys Leu Gln Glu Lys Asn Val Phe Leu Gln Ile Arg Leu
                85                  90                  95
Arg Gln Ser Phe Asn Asn Leu Ile Pro Ser Leu Pro Phe Arg Ile Asp
            100                 105                 110
Asn Thr Lys Lys Ile Thr Glu Met Lys Lys Thr Thr Leu Thr Gly Ser
        115                 120                 125
Ile Cys Ala Leu Leu Leu Phe Leu Gly Leu Ser Ala Asn Ala Gln Ser
    130                 135                 140
Lys Leu Lys Ile Lys Ser Ile Glu Ala Ala Thr Thr Phe Ser Ser Ala
145                 150                 155                 160
Thr Ala Gly Asn Gly Phe Gly Gly Asn Ile Phe Gly Met Asp Met Ser
                165                 170                 175
Ile Arg Met Arg Val His His Ser Ile Leu Pro Glu Gly Leu Asp Phe
            180                 185                 190
```

Ser Val Gly Ile His Glu Arg Arg Ala His Trp Glu Glu Ala Gly Ser
195 200 205

Pro Lys Leu Met Tyr Thr Asn Val Pro Ser Ile Ile Gly Ile Val Glu
210 215 220

Lys Val Ile Val Phe Glu Asp Ala Glu Asp Phe Phe Asp Lys Lys Ala
225 230 235 240

Leu Gly Arg Phe Leu Ile Ser Leu Gly Ile Ser Tyr Thr Lys His Leu
245 250 255

Gly Ala Tyr Trp Gly Trp Thr Asn Asp Ala His Ile Leu Phe Ser Pro
260 265 270

Ile Pro Lys Ser Lys Val His Tyr Asp Thr Tyr Thr Arg Ala Gly Ser
275 280 285

Asp Leu Val Leu Gln Ser Glu Asp Val Ala Thr Val Ser Asn Gly Phe
290 295 300

Ser Pro Gly Ile Gly Leu Lys Ser Ser Ile Trp Trp Lys Met Pro Ile
305 310 315 320

Lys Ser Lys Tyr Asp Phe Arg Leu Gly Phe Ser Leu Gly Tyr Glu Tyr
325 330 335

Leu Asn Leu Leu Tyr Pro Tyr Arg Asn Phe Lys Leu Asp Gly Asn Lys
340 345 350

Pro Leu Ser Ala Leu Ser Pro Arg Met Asn His Ile Gly His Val Gly
355 360 365

Phe Asn Phe Thr Val Gly Leu Trp Thr Asn
370 375

(2) INFORMATION FOR SEQ ID NO:73

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73

```
Ile Cys Gly Ser Lys Met Asn Leu Ser Gly Leu Gln Ser Phe Thr Met
1               5                   10                  15
Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu
            20                  25                  30
Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser
        35                  40                  45
Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
    50                  55                  60
Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
65                  70                  75                  80
Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
                85                  90                  95
Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr
            100                 105                 110
Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
        115                 120                 125
Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
    130                 135                 140
Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
145                 150                 155                 160
Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
                165                 170                 175
Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
            180                 185                 190
Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
        195                 200                 205
Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile
```

210 215 220

Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile

225 230 235 240

Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala

245 250 255

Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala

260 265 270

Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro

275 280 285

(2) INFORMATION FOR SEQ ID NO:74

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74

Gly Glu Tyr Pro Ala Asn Ser Asn Asp Lys Lys Glu Met Val Met Lys

1 5 10 15

Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu Ile Thr

20 25 30

Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp Ile Tyr

35 40 45

```
Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp Trp Gln
    50                  55                  60
Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val Ala Ser
65                  70                  75                  80
Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser Tyr Asp
                85                  90                  95
Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg Ser Ser
            100                 105                 110
Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys Pro Asn
        115                 120                 125
Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp Asp Gly
    130                 135                 140
Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser Ser Val
145                 150                 155                 160
Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr Thr Ser
                165                 170                 175
Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn Tyr Pro
            180                 185                 190
Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr Pro Gly
        195                 200                 205
Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn Pro Tyr
    210                 215                 220
Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser Tyr Tyr
225                 230                 235                 240
Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His Tyr Pro
                245                 250                 255
Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr Ser Tyr
            260                 265                 270
Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys Leu Gly
        275                 280                 285
Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys Asn Lys
    290                 295                 300
Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn Val Lys
305                 310                 315                 320
Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu Thr Val
                325                 330                 335
```

Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln Gln Asn
340 345 350

Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser Glu Arg
355 360 365

Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg Ser Asn
370 375 380

Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly Ser Met
385 390 395 400

Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
405 410

(2) INFORMATION FOR SEQ ID NO:75

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

Lys Arg Lys Ser Met Lys Arg Met Leu Leu Leu Leu Val Val Leu Leu
1 5 10 15

Tyr Gly Ile Ala Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp
20 25 30

Ser Leu Gln Val Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly

```
        35                  40                  45
Gly Phe Thr Tyr Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu
    50                  55                  60
Glu Val Gly Leu Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn
65                  70                  75                  80
Ala Asp Ser Phe Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn
                85                  90                  95
Met Ser Ser Pro Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala
            100                 105                 110
Asn Cys Tyr Met Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp
        115                 120                 125
Gln Asn Ser Arg His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser
    130                 135                 140
Asn Lys His Asn Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val
145                 150                 155                 160
Ser Ile Tyr Thr Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val
                165                 170                 175
Ala Tyr Glu Tyr Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val
            180                 185                 190
Met Tyr Asp His Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser
        195                 200                 205
Thr His Phe
    210
```

(2) INFORMATION FOR SEQ ID NO:76

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 786 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

```
Ile Val Tyr Leu Cys His Cys Met Asn His Arg Arg Ser Lys Thr Met
1               5                   10                  15
Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile Ala
            20                  25                  30
Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu Thr
        35                  40                  45
Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr Asn
    50                  55                  60
Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe Asn
65                  70                  75                  80
Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp Trp
                85                  90                  95
Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser His
            100                 105                 110
Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu Leu
        115                 120                 125
Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Cys Tyr Gly Ser
    130                 135                 140
Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val Leu
145                 150                 155                 160
Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr Ala
                165                 170                 175
Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu Asn
            180                 185                 190
Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe Leu
        195                 200                 205
Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys Tyr
    210                 215                 220
```

```
Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser Arg
225                 230                 235                 240
Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr Val
                245                 250                 255
Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp Gly
            260                 265                 270
Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser Phe
        275                 280                 285
Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser Phe
    290                 295                 300
Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu Glu
305                 310                 315                 320
Val Phe Lys Ser Val Gly Gly Asn Pro Ala Lys Ala Phe Ser Ala Ile
                325                 330                 335
Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val Glu
            340                 345                 350
Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala Leu
        355                 360                 365
Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly Glu
    370                 375                 380
Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp Arg
385                 390                 395                 400
Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro Leu
                405                 410                 415
Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr Leu
            420                 425                 430
Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu Tyr
        435                 440                 445
Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val Ile
    450                 455                 460
Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr Ala
465                 470                 475                 480
Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His Pro
                485                 490                 495
Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro Leu
            500                 505                 510
```

```
Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr Leu
        515                 520                 525
Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys Glu
    530                 535                 540
Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr Tyr
545                 550                 555                 560
Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser Phe
                565                 570                 575
Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn Pro
            580                 585                 590
Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro His
        595                 600                 605
Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe Ser
    610                 615                 620
Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr Asn
625                 630                 635                 640
Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys Glu
                645                 650                 655
Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His Phe
            660                 665                 670
Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr Met
        675                 680                 685
Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys Pro
    690                 695                 700
Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val Arg
705                 710                 715                 720
Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile Thr
                725                 730                 735
Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr Val
            740                 745                 750
Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser His
        755                 760                 765
Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn Arg
    770                 775                 780
Pro Arg
785
```

(2) INFORMATION FOR SEQ ID NO:77

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 953 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77

```
Ile Arg Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu
1               5                   10              15
Pro Val Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu
            20                  25                  30
Arg Pro Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala
        35                  40                  45
Leu Ser Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile
    50                  55                  60
Pro Asp Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser
65                  70                  75                  80
Met Arg Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile
                85                  90                  95
Val Glu Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg
            100                 105                 110
Ala Tyr Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu
```

```
        115                 120                 125
Glu Ala Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr
    130                 135                 140
Arg Tyr Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe
145                 150                 155                 160
Lys Asp Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe
                165                 170                 175
Arg Thr Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu
            180                 185                 190
Gly Tyr Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met
        195                 200                 205
Phe Met Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro
    210                 215                 220
His Phe Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp
225                 230                 235                 240
Ile Val Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro
                245                 250                 255
Ile Gly Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser
            260                 265                 270
Gly Ile Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr
        275                 280                 285
Leu Arg Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu
    290                 295                 300
Ala Leu Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala
305                 310                 315                 320
Gln Ser Lys Tyr Lys Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala
                325                 330                 335
Asn Tyr Leu Val Ser Lys Ser Gly Asp Lys Tyr Val Pro Gly Asp Tyr
            340                 345                 350
Ser Lys Thr Thr Ser Leu Asn Ile Arg Trp Thr His Ser Gln Asp Pro
        355                 360                 365
Lys Ala Asn Pro Leu Gln Thr Leu Ser Ala Asn Val Asn Phe Ala Thr
    370                 375                 380
Gly Ser Tyr Phe Gln Asn Ser Leu Asn Thr Thr Tyr Asp Val Asn Ala
385                 390                 395                 400
Arg Thr Ala Thr Thr Arg Ser Ser Ala Val Ser Tyr Ser Arg Lys Phe
```

```
                405                 410                 415
Pro Gly Thr Pro Phe Ser Ile Thr Gly Ser Met Asp Ile Ser Gln Asn
            420                 425                 430
Met Arg Asp Thr Thr Val Ser Leu Thr Leu Pro Asn Leu Ser Ile Asn
        435                 440                 445
Met Ser Thr Arg Tyr Pro Phe Lys Arg Lys Thr Arg Val Gly Pro Glu
    450                 455                 460
Arg Trp Tyr Glu Lys Leu Ser Val Gly Tyr Ser Gly Gln Leu Arg Asn
465                 470                 475                 480
Ser Ile Leu Thr Lys Glu Lys Asp Leu Leu Gln Ser Asn Leu Val Arg
                485                 490                 495
Asp Trp Lys Asn Gly Met Arg His Ser Val Pro Ile Ser Leu Thr Val
            500                 505                 510
Pro Leu Leu Asp Tyr Ile Asn Leu Thr Met Gly Val Asn Tyr Asn Glu
        515                 520                 525
Trp Trp Tyr Thr Lys Gly Ile Arg Lys Ser Trp Asn Glu Asp Lys Lys
    530                 535                 540
Thr Phe Leu Pro Ser Asp Thr Thr Tyr Lys Phe Arg Arg Leu Tyr Asp
545                 550                 555                 560
Tyr Ser Leu Ser Ala Gly Leu Ser Thr Thr Leu Tyr Gly Met Phe Lys
                565                 570                 575
Pro Trp Lys Pro Phe Ser Phe Gly Gly Asn Leu Ile Met Ile Arg His
            580                 585                 590
Arg Phe Thr Pro Thr Val Ser Phe Ser Tyr Met Pro Asp Phe Thr Lys
        595                 600                 605
Arg Arg Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly
    610                 615                 620
Lys Leu His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly
625                 630                 635                 640
Ala Pro Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn
                645                 650                 655
Asn Leu Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys
            660                 665                 670
Lys Ile Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met
        675                 680                 685
Phe Ala Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu
```

```
    690                 695                 700
Arg Leu Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro
705                 710                 715                 720
Tyr Leu Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr
                725                 730                 735
Lys Ser Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu
            740                 745                 750
Ile Ser Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu
        755                 760                 765
Ser Gly Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu
    770                 775                 780
Lys Lys Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp
785                 790                 795                 800
Ile Leu Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu
                805                 810                 815
Glu Arg Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala
            820                 825                 830
Tyr Ser Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala
        835                 840                 845
Thr Asp Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg
    850                 855                 860
Val Thr Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn
865                 870                 875                 880
Trp Ser Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile
                885                 890                 895
Thr Ser Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile
            900                 905                 910
Ser Ala Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val
        915                 920                 925
Ile Ser Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser
    930                 935                 940
Asn Arg Pro Ile Thr Asn Thr Trp Tyr
945                 950
```

(2) INFORMATION FOR SEQ ID NO:78

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 601 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78

```
Ser Asn Ser Ser Ser His Lys Trp Leu Ile Tyr Tyr His Ile Glu Lys
1               5                   10                  15
Thr Lys Ser Ile Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met
            20                  25                  30
Pro Val Ala Ser Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser
        35                  40                  45
Lys Asp Asn Arg Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg
    50                  55                  60
Asp Asp Ala Pro Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile
65                  70                  75                  80
Gln Ser Asp Met Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp
                85                  90                  95
Phe Gly Asn Ser Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu
            100                 105                 110
Phe Gly Ala Arg Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu
        115                 120                 125
Pro Glu Met Unk Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr
    130                 135                 140
```

```
His Trp Ala Glu Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser
145                 150                 155                 160
Gly Met Val Phe Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn
                165                 170                 175
Ala Val Arg Gly Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg
            180                 185                 190
Val Lys Gly Ile Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly
        195                 200                 205
Lys Val Phe Asn Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu
    210                 215                 220
Leu Asn Val Glu Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His
225                 230                 235                 240
Leu Ala Ile Gly Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp
                245                 250                 255
Ile Phe Val Gly Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu
            260                 265                 270
Asn Val Pro Ile Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu
        275                 280                 285
Ala Leu Tyr Ala Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp
    290                 295                 300
Asn Asp Tyr Ile Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser
305                 310                 315                 320
Tyr Ser Lys Lys Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu
                325                 330                 335
Asn Phe Ala Phe Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met
            340                 345                 350
Ile Asn Tyr Met Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala
        355                 360                 365
Ala Ile Tyr Pro Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln
    370                 375                 380
Gly Glu Leu Arg Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg
385                 390                 395                 400
Tyr Gly Thr Gly Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp
                405                 410                 415
Lys Lys Met Leu Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly
            420                 425                 430
```

```
Tyr Thr Val Ser Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile
        435                 440                 445
Asp Val Glu Ile Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu
    450                 455                 460
Thr Tyr Leu Asn Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala
465                 470                 475                 480
Gly Glu Lys Pro Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly
                485                 490                 495
Lys Tyr Lys Leu Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr
            500                 505                 510
Leu His Thr Lys Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu
        515                 520                 525
Leu Ser Ile Leu Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn
    530                 535                 540
Ile Gly Glu Thr Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr
545                 550                 555                 560
His Gly Ala His Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly
                565                 570                 575
Met Asn Cys Ser Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly
            580                 585                 590
Phe Tyr Leu Ser Tyr Ser Thr Asn Leu
        595                 600
```

(2) INFORMATION FOR SEQ ID NO:79

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 962 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79

```
Ala Ile Phe Val Val Ser Leu Gln Ile Glu Lys Ile Thr Glu Asn Lys
1               5                   10                  15
Tyr Asn Ser Asp Lys Ser Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln
            20                  25                  30
Ser Gly Leu Ala Ala Phe Val Ser Met Ala Thr Ala Leu Thr Ala Ser
        35                  40                  45
Ala Gln Ile Ser Phe Gly Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser
    50                  55                  60
Ala Gly Thr His Ser Phe Asp Asp Ala Met Thr Ile Arg Leu Thr Pro
65                  70                  75                  80
Asp Phe Asn Pro Glu Asp Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln
                85                  90                  95
Arg Asp Gly Arg Pro Val Arg Ile Gly Gln Val Ile Pro Val Asp Val
            100                 105                 110
Asp Phe Ala Ser Lys Ala Ser His Ile Ser Ser Ile Gly Asp Val Asp
        115                 120                 125
Val Tyr Arg Leu Gln Phe Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu
    130                 135                 140
Tyr Tyr Asp Ala Phe Asn Ile Pro Glu Gly Gly Arg Leu Tyr Ile Tyr
145                 150                 155                 160
Thr Pro Asp His Glu Ile Val Leu Gly Ala Tyr Thr Asn Ala Thr His
                165                 170                 175
Arg Arg Asn Gly Ala Phe Ala Thr Glu Pro Val Pro Gly Ser Glu Leu
            180                 185                 190
Ile Met Asp Tyr Glu Val Ser Arg Gly Gly Thr Leu Pro Asp Ile Lys
        195                 200                 205
Ile Ser Gly Ala Gly Tyr Ile Phe Asp Lys Val Gly Gly Arg Pro Val
    210                 215                 220
Thr Asp Asn His Tyr Gly Ile Gly Glu Asp Asp Ser Asp Ser Asp Cys
```

```
225                 230                 235                 240
Glu Ile Asn Ile Asn Cys Pro Glu Gly Ala Asp Trp Gln Ala Glu Lys
                245                 250                 255
Asn Gly Val Val Gln Met Ile Met Val Lys Gly Gln Tyr Ile Ser Met
            260                 265                 270
Cys Ser Gly Asn Leu Leu Asn Asn Thr Lys Gly Asp Phe Thr Pro Leu
        275                 280                 285
Ile Ile Ser Ala Gly His Cys Ala Ser Ile Thr Thr Asn Phe Gly Val
    290                 295                 300
Thr Gln Ser Glu Leu Asp Lys Trp Ile Phe Thr Phe His Tyr Glu Lys
305                 310                 315                 320
Arg Gly Cys Ser Asn Gly Thr Leu Ala Ile Phe Arg Gly Asn Ser Ile
                325                 330                 335
Ile Gly Ala Ser Met Lys Ala Phe Leu Pro Ile Lys Gly Lys Ser Asp
            340                 345                 350
Gly Leu Leu Leu Gln Leu Asn Asp Glu Val Pro Leu Arg Tyr Arg Val
        355                 360                 365
Tyr Tyr Asn Gly Trp Asp Ser Thr Pro Asp Ile Pro Ser Ser Gly Ala
    370                 375                 380
Gly Ile His His Pro Ala Gly Asp Ala Met Lys Ile Ser Ile Leu Lys
385                 390                 395                 400
Lys Thr Pro Ala Leu Asn Thr Trp Ile Ser Ser Ser Gly Ser Gly Gly
                405                 410                 415
Thr Asp Asp His Phe Tyr Phe Lys Tyr Asp Gln Gly Gly Thr Glu Gly
            420                 425                 430
Gly Ser Ser Gly Ser Ser Leu Phe Asn Gln Asn Lys His Val Val Gly
        435                 440                 445
Thr Leu Thr Gly Gly Ala Gly Asn Cys Gly Gly Thr Glu Phe Tyr Gly
    450                 455                 460
Arg Leu Asn Ser His Trp Asn Glu Tyr Ala Ser Asp Gly Asn Thr Ser
465                 470                 475                 480
Arg Met Asp Ile Tyr Leu Asp Pro Gln Asn Asn Gly Gln Thr Thr Ile
                485                 490                 495
Leu Asn Gly Thr Tyr Arg Asp Gly Tyr Lys Pro Leu Pro Ser Val Pro
            500                 505                 510
Arg Leu Leu Leu Gln Ser Thr Gly Asp Gln Val Glu Leu Asn Trp Thr
```

```
        515                 520                 525
Ala Val Pro Ala Asp Gln Tyr Pro Ser Ser Tyr Gln Val Glu Tyr His
    530                 535                 540
Ile Phe Arg Asn Gly Lys Glu Ile Ala Thr Thr Lys Glu Leu Ser Tyr
545                 550                 555                 560
Ser Asp Ala Ile Asp Glu Ser Ile Ile Gly Ser Gly Ile Ile Arg Tyr
                565                 570                 575
Glu Val Ser Ala Arg Phe Ile Tyr Pro Ser Pro Leu Asp Gly Val Glu
            580                 585                 590
Ser Tyr Lys Asp Thr Asp Lys Thr Ser Ala Asp Leu Ala Ile Gly Asp
        595                 600                 605
Ile Gln Thr Lys Leu Lys Pro Asp Val Thr Pro Leu Pro Gly Gly Gly
    610                 615                 620
Val Ser Leu Ser Trp Lys Val Pro Phe Leu Ser Gln Leu Val Ser Arg
625                 630                 635                 640
Phe Gly Glu Ser Pro Asn Pro Val Phe Lys Thr Phe Glu Val Pro Tyr
                645                 650                 655
Val Ser Ala Ala Ala Ala Gln Thr Pro Asn Pro Pro Val Gly Val Val
            660                 665                 670
Ile Ala Asp Lys Phe Met Ala Gly Thr Tyr Pro Glu Lys Ala Ala Ile
        675                 680                 685
Ala Ala Val Tyr Val Met Pro Ser Ala Pro Asp Ser Thr Phe His Leu
    690                 695                 700
Phe Leu Lys Ser Asn Thr Asn Arg Arg Leu Gln Lys Val Thr Thr Pro
705                 710                 715                 720
Ser Asp Trp Gln Ala Gly Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro
                725                 730                 735
Phe Pro Val Asn Asn Asp His Met Leu Phe Ala Gly Ile Arg Met Pro
            740                 745                 750
Asn Lys Tyr Lys Leu Asn Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp
        755                 760                 765
Asn Leu Phe Ser Ile Thr Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val
    770                 775                 780
Ser Phe Glu Gly Tyr Gly Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile
785                 790                 795                 800
Lys Tyr Leu Val Val Asn Thr Asp Ala Pro Lys Ile Asp Met Ser Leu
```

805 810 815
Val Gln Glu Pro Tyr Ala Lys Gly Thr Asn Val Ala Pro Phe Pro Glu
820 825 830
Leu Val Gly Ile Tyr Val Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln
835 840 845
Asp Pro Ser Val Thr Thr Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp
850 855 860
Glu Tyr Glu Ile Lys Leu Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly
865 870 875 880
Val Ala Gln Ile Glu Asn Asn Asn Ala Val Val Ala Tyr Pro Ser Val
885 890 895
Val Thr Asp Arg Phe Ser Ile Lys Asn Ala His Met Val His Ala Ala
900 905 910
Ala Leu Tyr Ser Leu Asp Gly Lys Gln Val Arg Ser Trp Asn Asn Leu
915 920 925
Arg Asn Gly Val Thr Phe Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr
930 935 940
Met Leu Val Met Gln Thr Ala Asn Gly Pro Val Ser Gln Lys Ile Val
945 950 955 960
Lys Gln

(2) INFORMATION FOR SEQ ID NO:80

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1312 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

Lys Arg Val Asp Ser Tyr Glu Cys Arg Gln Lys Ala Cys Lys Cys Ala
1 5 10 15

Ile Cys Val Ile Gln Lys Phe Thr Asn Val Lys Leu Asn Asp Met Arg
20 25 30

Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly Leu Gln
35 40 45

Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu Pro Ser
50 55 60

Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu Val Val
65 70 75 80

Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln Val Phe
85 90 95

Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu Gly Glu
100 105 110

Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu Phe Ser
115 120 125

Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe Asp Asn
130 135 140

Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu Pro Glu
145 150 155 160

Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp Tyr Tyr
165 170 175

Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser Gln Asp
180 185 190

Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr Pro Phe
195 200 205

Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys Ile Glu
210 215 220

Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys Asn Thr
225 230 235 240

```
Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr Glu Ala
                245                 250                 255
Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg Gly Thr
            260                 265                 270
Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln Asn Cys
        275                 280                 285
Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln Gln Pro
    290                 295                 300
His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr Asn Gly
305                 310                 315                 320
Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser Phe Pro
                325                 330                 335
Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn Phe Ile
            340                 345                 350
Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp Gly Lys
        355                 360                 365
Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr Leu Ala
    370                 375                 380
Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn Val Ser
385                 390                 395                 400
Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser Asp Tyr
                405                 410                 415
Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu Phe Ile
            420                 425                 430
Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu Ile Glu
        435                 440                 445
Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His Lys Asn
    450                 455                 460
Ile Leu Tyr Ala Glu Gly Lys Gly Cys Asp Ala Pro Ile Leu Arg Leu
465                 470                 475                 480
Phe Leu Lys Glu Ile Ala Ser Gly Tyr Thr Val Asn Ser Ile Leu Lys
                485                 490                 495
Ser Asn Gln Val Ser Ala Ile Asp Ser Ile Phe Asp Cys Leu Asn Asn
            500                 505                 510
Gly Ser His His Phe Tyr Phe Asn Thr His Gly Met Pro Thr Val Trp
        515                 520                 525
```

```
Gly Ile Gly Gln Gly Leu Asp Val Asn Thr Leu Thr Ala Arg Leu Asn
    530                 535                 540
Asn Thr Ser Ser Gln Gly Leu Cys Thr Ser Leu Ser Cys Ser Ser Ala
545                 550                 555                 560
Val Ala Asp Ser Thr Ile Arg Ser Leu Gly Glu Val Leu Thr Thr Tyr
                565                 570                 575
Ala Pro Asn Lys Gly Phe Ser Ala Phe Leu Gly Gly Ser Arg Ala Thr
            580                 585                 590
Gln Tyr Ala Val Tyr Leu Glu Gly Pro Cys Pro Pro Ser Glu Phe Tyr
        595                 600                 605
Glu Tyr Leu Pro Tyr Ser Leu Tyr His Asn Leu Ser Thr Val Val Gly
    610                 615                 620
Glu Met Leu Leu Ser Ser Ile Ile Asn Thr Asn Ser Val Asp Thr Tyr
625                 630                 635                 640
Ser Lys Phe Asn Phe Asn Leu Leu Gly Asp Pro Ala Leu Asn Ile Met
                645                 650                 655
Ala His Gly Met Glu Val Ser Asn Cys Ile Thr Leu Pro Asn Asn Thr
            660                 665                 670
Ile Ile Ser Ser Pro Ile Thr Ile Lys Asn Gly Gly Cys Leu Lys Ile
        675                 680                 685
Pro Glu Lys Gly Val Leu His Phe Thr Asn Asn Gly Ser Ile Gln Val
    690                 695                 700
Met Ser Gly Gly Thr Leu Glu Ile Gly Asn Gln Ala Lys Ile Ser Gly
705                 710                 715                 720
Glu Thr Gly Ala Asn Pro Thr Phe Ile Thr Val Tyr Gly Asp Gly Leu
                725                 730                 735
Ala Ile Asn Lys Gln Val Glu Ile Asp Asn Ile Asp Arg Leu Asn Leu
            740                 745                 750
Phe Ser Thr His Ser Val Met Pro Lys Phe His Phe Asp Ser Val Lys
        755                 760                 765
Phe Asn Ser Ala Pro Leu Tyr Thr Thr Asn Cys Ile Val Glu Ile Ser
    770                 775                 780
Asn Cys Glu Phe Thr Asn Arg Ser Asp Ile Ile Ser Lys Asn Cys Asp
785                 790                 795                 800
Leu Ser Val Glu Asn Ser Met Phe Ser Ser Ser Gly Ile Thr Val Phe
                805                 810                 815
```

```
Lys Pro Met Ala Thr Ser Ser Ile Thr Gly Leu Ser Thr Lys Ala Lys
            820                 825                 830
Ile Thr Asp Asn Thr Phe Phe Ala Thr Gly Asn Phe Ala Tyr His Ile
        835                 840                 845
Thr Asn Thr Pro Gly Leu Thr Ala Thr Ser Asn Ala Ala Ile Lys Leu
    850                 855                 860
Asp Asn Ile Pro Glu Tyr Tyr Ile Ser Gly Asn Lys Ile Val Asn Cys
865                 870                 875                 880
Asp Glu Ala Leu Val Leu Asn Asn Ser Gly Asn Arg Thr Asn Arg Leu
                885                 890                 895
His Asn Ile Thr Arg Asn Val Ile Lys Asn Cys Arg Ile Gly Ser Thr
            900                 905                 910
Leu Tyr Asn Ser Tyr Gly Ile Tyr Asn Arg Asn Lys Ile Ser Asn Asn
        915                 920                 925
His Ile Gly Val Arg Leu Leu Asn Asn Ser Cys Phe Tyr Phe Asp Asn
    930                 935                 940
Ala Pro Val Ile Asn Glu Glu Asp Lys Gln Thr Phe Ile Ser Asn Arg
945                 950                 955                 960
Thr Trp Gln Leu Tyr Ser Ser Asn Gly Thr Phe Pro Leu Asn Phe His
                965                 970                 975
Tyr Asn Ser Leu Gln Gly Gly Asp Thr Asp Thr Trp Ile Tyr Asn Asp
            980                 985                 990
Thr Tyr Thr Asn Arg Tyr Ile Asp Val Ser Asn Asn His Trp Gly Asn
        995                 1000                1005
Asn Asp Leu Phe Asp Pro Asn Gln Val Phe Asn Thr Pro Asp Leu Phe
    1010                1015                1020
Ile Trp Ile Pro Phe Trp Asp Gly Leu Pro Asn Gly Arg Ser Gly Asn
1025                1030                1035                1040
Ser Ser Ala Glu Ala Val Glu Phe Gln Thr Ala Leu Asp Cys Ile Gly
                1045                1050                1055
Asn Ser Asp Tyr Leu Ser Ala Lys Val Ala Leu Lys Met Met Val Glu
            1060                1065                1070
Thr Tyr Pro Glu Ser Asp Phe Ala Ile Ala Ala Leu Lys Glu Leu Phe
        1075                1080                1085
Arg Ile Glu Lys Met Ser Gly Asn Asp Tyr Glu Gly Leu Lys Asp Tyr
    1090                1095                1100
```

Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe Pro Thr

1105 1110 1115 1120

Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn Tyr Gln

1125 1130 1135

Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile Ser Tyr

1140 1145 1150

Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr Trp Asn

1155 1160 1165

Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn Ile Leu

1170 1175 1180

Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val Lys Asn

1185 1190 1195 1200

Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu Pro Pro

1205 1210 1215

Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile Ser Ile

1220 1225 1230

Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr Thr Asp

1235 1240 1245

Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly Ala Ser

1250 1255 1260

Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr Tyr Ser

1265 1270 1275 1280

Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu Val Thr

1285 1290 1295

Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg Ile Lys

1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:81

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 938 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

```
Ser Glu Asn Tyr Arg Tyr Gly Lys Ile Thr Asn Gln Ile Met Ala Ile
1               5                   10                  15
Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser
            20                  25                  30
Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn
        35                  40                  45
Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
    50                  55                  60
Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
65                  70                  75                  80
Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
                85                  90                  95
Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly
            100                 105                 110
Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
        115                 120                 125
Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
    130                 135                 140
His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe
145                 150                 155                 160
Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val
                165                 170                 175
Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala
            180                 185                 190
Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu
```

```
        195                 200                 205
Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr
    210                 215                 220
Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp
225                 230                 235                 240
Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu
                245                 250                 255
Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln
            260                 265                 270
Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu
        275                 280                 285
Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp
    290                 295                 300
Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr
305                 310                 315                 320
Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly
                325                 330                 335
Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr
            340                 345                 350
Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser
        355                 360                 365
Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn
    370                 375                 380
Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp
385                 390                 395                 400
Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met
                405                 410                 415
Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu
            420                 425                 430
Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile
        435                 440                 445
Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys
    450                 455                 460
Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr
465                 470                 475                 480
Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile
```

```
                485                 490                 495
Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu
            500                 505                 510
Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala Gly Tyr Asn
        515                 520                 525
Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val
    530                 535                 540
Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp Gln Val Glu
545                 550                 555                 560
Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln
                565                 570                 575
Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp Ile Ile Leu
            580                 585                 590
Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp Leu Leu Ile
        595                 600                 605
Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro Trp Thr Met
    610                 615                 620
Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser Tyr Leu Pro
625                 630                 635                 640
Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr Pro Arg Leu
                645                 650                 655
Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val
            660                 665                 670
Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala
        675                 680                 685
Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala
    690                 695                 700
Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys
705                 710                 715                 720
Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu
                725                 730                 735
Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro
            740                 745                 750
Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu
        755                 760                 765
Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys
```

770 775 780
Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu
785 790 795 800
Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr
805 810 815
Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala
820 825 830
Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn
835 840 845
Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys
850 855 860
Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser
865 870 875 880
Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile
885 890 895
Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg
900 905 910
Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr
915 920 925
Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
930 935

(2) INFORMATION FOR SEQ ID NO:82

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1251 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

```
Lys Trp Lys Leu Ala Cys Ala Phe Asp Cys Ala Cys Cys Phe Asp Pro
1               5                   10                  15
Phe Val Val Thr Asn Glu Val Ile Ile Met Met Lys Arg Tyr Thr Ile
            20                  25                  30
Ile Leu Ala Val Phe Leu Leu Phe Cys Thr Val Phe Thr Phe Gln Ile
        35                  40                  45
Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp Val Glu Lys Pro Trp Ile
    50                  55                  60
Gln Lys His Ser Met Asp Ser Lys Leu Val Pro Ala Asn Lys Gly Asn
65                  70                  75                  80
Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser Val Ser Glu His Ser Asp
                85                  90                  95
Leu Val Ile Ser Pro Val Asn Glu Ile Arg Pro Ala Asn Arg Phe Pro
            100                 105                 110
Ser His Arg Lys Ser Phe Phe Ala Glu Asn Leu Arg Ala Ser Pro Pro
        115                 120                 125
Val Val Pro Val Ala Val Asp Lys Tyr Ala Val Pro Val Ala Asn Pro
    130                 135                 140
Met Asp Pro Glu Asn Pro Asn Ala Trp Asp Val Thr Leu Lys Ile Thr
145                 150                 155                 160
Thr Lys Ala Val Thr Val Pro Val Asp Val Val Met Val Ile Asp Gln
                165                 170                 175
Ser Ser Ser Met Gly Gly Gln Asn Ile Ala Arg Leu Lys Ser Ala Ile
            180                 185                 190
Ala Ser Gly Gln Arg Phe Val Lys Lys Met Leu Pro Lys Gly Thr Ala
        195                 200                 205
Thr Glu Gly Val Arg Ile Ala Leu Val Ser Tyr Asp His Glu Pro His
    210                 215                 220
Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala Phe Leu Cys Gln Lys Ile
225                 230                 235                 240
```

```
Arg Ala Leu Thr Pro Ile Trp Gly Thr His Thr Gln Gly Gly Leu Lys
                245                 250                 255
Met Ala Arg Asn Ile Met Ala Thr Ser Thr Ala Val Asp Lys His Ile
            260                 265                 270
Ile Leu Met Ser Asp Gly Leu Ala Thr Glu Gln Tyr Pro Val Lys Asn
        275                 280                 285
Val Thr Thr Ala Asp Phe Ile Gly Lys Thr Gly Asn Ala Asn Asp Pro
    290                 295                 300
Ile Asp Leu Val Ile Gln Gly Ala Ile Asn Phe Pro Thr Asn Tyr Val
305                 310                 315                 320
Ser Asn Asn Pro Ser Thr Pro Leu Thr Pro Asn Tyr Pro Thr His Ser
                325                 330                 335
Ser Lys Val Gly Arg Arg Asn Leu Pro Glu Ser Lys Phe Asp Tyr Ser
            340                 345                 350
Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly Val Ala Gly Ala Leu Val
        355                 360                 365
Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr Tyr Tyr Phe Pro Cys Asn
    370                 375                 380
Ala Ala Ile Asn Glu Ala Gln Phe Ala Lys Asn Ser Gly Tyr Thr Ile
385                 390                 395                 400
His Thr Ile Gly Tyr Asp Leu Gly Asp Phe Ala Leu Ala Asn Asn Ser
                405                 410                 415
Leu Lys Leu Thr Ala Thr Asp Glu Asn His Phe Phe Thr Ala Thr Pro
            420                 425                 430
Ala Asn Leu Ala Ala Ala Phe Asp Asn Ile Ala Gln Thr Ile Asn Ile
        435                 440                 445
Gly Ile Gln Arg Gly Glu Val Thr Asp Phe Val Ala Pro Gly Phe Ile
    450                 455                 460
Val Lys Asn Leu Thr Gln Ser Gly Asp Val Thr His Leu Leu Asn Val
465                 470                 475                 480
Ser Asn Gly Thr Val His Tyr Asp Val Ser Thr Lys Lys Leu Thr Trp
                485                 490                 495
Thr Thr Gly Thr Ile Leu Ser Ser Ser Glu Ala Thr Ile Thr Tyr Arg
            500                 505                 510
Ile Tyr Ala Asp Leu Asp Tyr Ile Gln Asn Asn Asp Ile Pro Val Asn
        515                 520                 525
```

```
Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly Gly Phe Asp Thr Asn Thr
    530                 535                 540
Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn Gly Glu Pro Asn Gln Gln
545                 550                 555                 560
Leu Ile Phe Pro Arg Pro Thr Val Lys Leu Gly Tyr Gly Val Ile Lys
                565                 570                 575
Arg His Tyr Val Leu Val Asn Lys Asp Gly Gln Pro Ile Gln Ala Asn
            580                 585                 590
Gly Thr Val Val Ser Ser Leu Ser Glu Ala His Val Leu Gln Ser Gln
        595                 600                 605
Asp Phe Phe Leu Pro Ser Gly Gly Gly His Ile Val Pro Lys Trp Ile
    610                 615                 620
Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln Tyr Tyr Ser Val Pro Pro
625                 630                 635                 640
Thr Asn Thr Val Ile Thr Thr Ala Asp Gly Lys Arg Tyr Arg Phe Val
                645                 650                 655
Glu Val Pro Gly Ser Thr Pro Asn Pro Gly Gln Ile Gly Ile Ser Trp
            660                 665                 670
Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala Tyr Lys Leu Leu Asn Tyr
        675                 680                 685
Trp Met Gly Gly Thr Thr Asp Gln Gln Ser Glu Trp Asp Val Thr Ser
    690                 695                 700
Asn Trp Thr Gly Ala Gln Val Pro Leu Thr Gly Glu Asp Val Glu Phe
705                 710                 715                 720
Ala Thr Thr Glu Asn Phe Gly Ser Pro Ala Val Ala Asp Leu His Val
                725                 730                 735
Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn Leu Ile Asn Asn Ser Asp
            740                 745                 750
Lys Asp Leu Val Val Thr Thr Ser Ser Gln Leu Thr Ile Asn Gly Val
        755                 760                 765
Val Glu Asp Asn Asn Pro Asn Val Gly Thr Ile Val Val Lys Ser Ser
    770                 775                 780
Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe Ala Asn Pro Gly Tyr Asn
785                 790                 795                 800
Gln Asn Val Gly Gly Thr Val Glu Phe Tyr Asn Gln Gly Tyr Asp Cys
                805                 810                 815
```

```
Ala Asp Cys Gly Met Tyr Arg Arg Ser Trp Gln Tyr Phe Gly Ile Pro
            820                 825                 830
Val Asn Glu Ser Gly Phe Pro Ile Asn Asp Val Gly Gly Asn Glu Thr
        835                 840                 845
Val Asn Gln Trp Val Glu Pro Phe Asn Gly Asp Lys Trp Arg Pro Ala
    850                 855                 860
Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys Phe Lys Gly Tyr Gln Ile
865                 870                 875                 880
Thr Asn Asp Val Gln Ala Gln Pro Thr Gly Val Tyr Ser Phe Lys Gly
                885                 890                 895
Met Ile Cys Val Cys Asp Ala Phe Leu Asn Leu Thr Arg Thr Ser Gly
            900                 905                 910
Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly Asn Ser Tyr Thr Gly Ala
        915                 920                 925
Ile Asp Ile Lys Gln Gly Ile Val Phe Pro Pro Glu Val Glu Gln Thr
    930                 935                 940
Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp Gln Trp Arg Lys Leu Asn
945                 950                 955                 960
Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly Gln Tyr Leu Ser Val Pro
                965                 970                 975
Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro Asp Arg Ile Pro Ser Met
            980                 985                 990
His Ser Phe Leu Val Lys Met Gln Asn Gly Ala Ser Cys Thr Leu Unk
        995                 1000                1005
Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr Thr Val Asn Asn Gly Asn
    1010                1015                1020
Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn Ser Gly Ser Ala Asn Met
1025                1030                1035                1040
Pro Ser Leu Val Met Asp Val Leu Gly Asn Glu Ser Ala Asp Arg Leu
                1045                1050                1055
Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe Gly Phe Asp Asn Gly Trp
            1060                1065                1070
Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu Ser Gln Leu Tyr Ala Met
        1075                1080                1085
Ser Asp Ile Gly Asn Asp Lys Phe Gln Val Ala Gly Val Pro Glu Leu
    1090                1095                1100
```

```
Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp Lys Asp Gly Gln Tyr Thr
1105                1110                1115                1120
Leu Glu Phe Ala Leu Ser Asp His Phe Ala Lys Gly Ala Val Tyr Leu
                1125                1130                1135
His Asp Leu Gln Ser Gly Ala Lys His Arg Ile Thr Asn Ser Thr Ser
            1140                1145                1150
Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser Gly Ala Arg Phe Arg Leu
        1155                1160                1165
Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp Ser His Val Val Ser Thr
    1170                1175                1180
Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln Asp Ala Leu Asp Cys Thr
1185                1190                1195                1200
Val Thr Leu Phe Thr Ile Glu Gly Lys Leu Leu Arg Arg Leu Lys Val
                1205                1210                1215
Leu Ala Gly His Arg Glu Val Met Lys Val Gln Thr Gly Gly Ala Tyr
            1220                1225                1230
Ile Val His Leu Gln Asn Ala Phe Thr Asn Asp Val His Lys Val Leu
        1235                1240                1245
Val Glu Tyr
    1250
```

(2) INFORMATION FOR SEQ ID NO:83

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

```
Thr Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp
1               5                   10                  15
Phe Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu
            20                  25                  30
Gly Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr
        35                  40                  45
His Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr
    50                  55                  60
Arg Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala
65                  70                  75                  80
Val Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly
                85                  90                  95
Leu Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly
            100                 105                 110
Leu Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val
        115                 120                 125
Arg Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala
    130                 135                 140
Gln Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser
145                 150                 155                 160
Val Phe Asn Glu Ser Met Lys Val Glu Val Val Val Leu Pro Val Phe
                165                 170                 175
Glu Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe
            180                 185                 190
Ser Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu
        195                 200                 205
Ala Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg
    210                 215                 220
Trp Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His
225                 230                 235                 240
Thr Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr
```

```
                245                 250                 255
Glu Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly
            260                 265                 270
Asp Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala
        275                 280                 285
Phe Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu
    290                 295                 300
Gly Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro
305                 310                 315                 320
Gly Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg
                325                 330                 335
Tyr Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu
            340                 345                 350
Asn Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe
        355                 360                 365
Thr Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala
    370                 375                 380
Asp Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp
385                 390                 395                 400
Phe Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser
                405                 410                 415
Glu Leu Trp Phe Lys Ala Arg Tyr Ser Phe
            420                 425
```

(2) INFORMATION FOR SEQ ID NO:84

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

```
Arg Gly Ser Ser Ser Gly Ile Ser Ala Arg Gly Arg Asp Met Arg Ser
1               5                   10                  15
Leu Phe Leu Ser Ala Leu Arg Ser Ser Ser Leu His Gly Ser Glu Arg
            20                  25                  30
Arg Ser Arg Ile Ser Ser Ser Val Val Met Ser Ile Arg Gln Lys Ile
        35                  40                  45
Arg Leu Phe His Leu Ser Val Cys Ala Gln Thr His Asp His Leu Ile
    50                  55                  60
Glu Ile His Leu Val Cys Ile Glu Phe Gly Ala Ile Asp Thr Asp Glu
65                  70                  75                  80
Phe Arg Leu Ser Ser His Ala Tyr Thr Thr Ser Pro Thr His Thr Gly
                85                  90                  95
Ala Ile His His Asn Cys Ile Glu Arg Ser Tyr Gly Arg Tyr Leu Val
            100                 105                 110
Thr Phe Gly Gln Glu Arg Asn Glu Leu His His His Ser Arg Pro Asp
        115                 120                 125
Arg Asn Ala Glu Val Tyr Arg Phe Pro Phe Asp Asn Ala Phe His Ser
    130                 135                 140
Ile Arg Tyr Glu Ala Phe Arg Pro Ile Arg Pro Ile Val Cys His Asp
145                 150                 155                 160
Asp His Phe Ile Ala Ile Gly Ser His Leu Phe Phe Lys Asp Asn Gln
                165                 170                 175
Ile Phe Ser Ser Gly Ser Gln Tyr Asp Asn Tyr Thr Val Ala Cys Phe
            180                 185                 190
Val Glu Ser Leu His Asp Arg Glu Gln Arg Ser His Thr His Thr Ala
        195                 200                 205
Ser Gly Thr Asn His Cys Ala Asp Leu Phe Asp Met Arg Thr Leu Ser
    210                 215                 220
```

Gln Arg Thr Tyr His Ile Arg Asp Ile Val Ala Asp Phe Glu Phe Gly
225 230 235 240

Gln Phe Leu Gly Arg Phe Ala His Gly Leu Asn His
245 250

(2) INFORMATION FOR SEQ ID NO:85

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

Ile Ile Tyr Arg Ser Thr Met Lys Leu Leu Leu Tyr Leu Leu Leu Val
1 5 10 15

Leu Ser Thr Leu Ser Pro Met Tyr Ser Gln Met Leu Phe Ser Glu Asn
20 25 30

Leu Thr Met Asn Ile Asp Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu
35 40 45

Pro Val Leu Asp Phe Lys Thr Glu Lys Glu Asn Val Phe Thr Phe Lys
50 55 60

Asn Thr Ala Asn Leu Asn Leu Leu Ile Lys His Gly Gln Val Ile Asn
65 70 75 80

Leu Ile Asn Lys Leu Glu Phe Ser Thr Tyr Gly Asn Lys Val Thr Val

```
                85                  90                  95
Ser Gly Gly Tyr Val His Thr Glu Tyr Arg Tyr Leu Leu His His Val
            100                 105                 110
Phe Glu Val Tyr Pro Tyr Val Glu Ser Gln Trp Ala Glu Ser Arg Gly
        115                 120                 125
Met Lys Tyr Lys Val Ser Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val
    130                 135                 140
Asn Ser Asp Asn Cys Leu Met Phe Ala Thr Leu Gly Val Phe Phe Glu
145                 150                 155                 160
Phe Glu Lys Trp Glu Gln Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr
                165                 170                 175
Ala Tyr Ser Arg Ser Ile Lys Ser His Leu Ser Ile Ser Phe Arg His
            180                 185                 190
Arg Leu Gly Glu His Trp Glu Phe Thr Thr Thr Ala Ile His Gln Gly
        195                 200                 205
Lys Pro Asp Ser Tyr Phe Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp
    210                 215                 220
Leu Lys Tyr His Ile Thr Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg
225                 230                 235                 240
Ile Ile Tyr Asp Thr Ala Pro Ile Val Pro Val Arg Lys Asp Tyr Asn
                245                 250                 255
Thr Val Asp Val Gly Ile Asp Ile Ser Phe
            260                 265
```

(2) INFORMATION FOR SEQ ID NO:86

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86

```
Glu Thr Asn Ser Trp Val Ser Ser Asp Cys Asn Ser Thr Thr Met Lys
1               5                   10                  15
Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu Thr Gly
            20                  25                  30
Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr Ala Phe
        35                  40                  45
Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser Ala Tyr
    50                  55                  60
Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Gly Ser Ile Thr Arg
65                  70                  75                  80
Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu Asn Leu
                85                  90                  95
Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg Trp Met
            100                 105                 110
Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn Pro Ala
        115                 120                 125
Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala Ala Ala
    130                 135                 140
Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met Asp Asn
145                 150                 155                 160
Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly Gly Ile
                165                 170                 175
Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu Tyr Thr
            180                 185                 190
Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser Glu Thr
        195                 200                 205
Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe Gly Ile
    210                 215                 220
```

```
Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe Leu Leu
225                 230                 235                 240
Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly Lys Phe
                245                 250                 255
Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg Asn Phe
            260                 265                 270
Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser Ser Leu
        275                 280                 285
Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile Gly Phe
    290                 295                 300
Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn Thr Gly
305                 310                 315                 320
Arg Arg Thr Ser Leu Tyr Tyr His Asp
                325
```

(2) INFORMATION FOR SEQ ID NO:87

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 814 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87

```
Pro Arg Phe His Pro Gly Gly Thr His Ala Gln Leu Cys Arg Asn Gly
```

```
1               5                   10                  15
Arg Arg Asn Gln Lys Ser Asn Gln Ser Ser Cys Phe Gly Gly Gly Thr
            20                  25                  30
Ala Pro Arg Phe Phe Ile Met Cys Lys Ile Arg Phe Ser Leu Leu Gln
        35                  40                  45
Ala Leu Val Val Cys Leu Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln
    50                  55                  60
Glu Glu Gly Ile Trp Asn Thr Leu Leu Ala Ile His Lys Thr Glu Lys
65                  70                  75                  80
Ala Val Glu Thr Pro Lys Lys Val Phe Ala Val Ala Asn Gly Val Leu
                85                  90                  95
Tyr Ser Val Gly Lys Glu Ala Pro His Glu Ala Lys Ile Phe Asp Arg
            100                 105                 110
Ile Ser Gly Leu Ser Asp Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu
        115                 120                 125
Gln Leu Lys Ser Leu Val Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile
    130                 135                 140
Leu Asp Glu Ala Gly Arg Val Thr Asn Val Pro Ala Leu Lys Asp Asn
145                 150                 155                 160
Ile Asp Leu Ile Asp Lys Thr Leu Asn Arg Leu Leu Ile Val Gly Asn
                165                 170                 175
Arg Ala Tyr Leu Ala Gly Gly Phe Gly Leu Ser Val Leu Asp Val Ala
            180                 185                 190
Glu Ala Arg Ile Pro Ala Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp
        195                 200                 205
Val Ala Lys Leu Asp Asn Asp Arg Leu Leu Met Leu Lys Glu Gly Gln
    210                 215                 220
Leu Phe Ile Gly Lys Glu Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp
225                 230                 235                 240
Thr Ala Leu Ser Leu Asn Leu Pro Met Gly Ser Val Thr Gly Leu Gly
                245                 250                 255
Ile Val Gly Glu Asp Ile Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr
            260                 265                 270
Val Ala Ala Asn Gln Ser Phe Glu Pro Glu Leu Leu Leu Ser Ser Ser
        275                 280                 285
Ala Asp Ser Arg Leu Tyr Val Thr Asp Arg Gly Leu Phe Ile Cys Ala
```

```
    290                 295                 300
Glu Asn Arg Ile Tyr Phe Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe
305                 310                 315                 320
Pro Ile Ala Asp Val Leu Gly Val Gly Ala Met Asn Glu Ser Asn Thr
                325                 330                 335
Ala Tyr Ile Ala Leu Gly Glu Glu Gly Leu Ala Ser Leu Leu Leu Ala
            340                 345                 350
Glu Gly Ser Thr Ala Glu Ala Met Pro Val Ala Phe Asp Gly Pro Gly
        355                 360                 365
Asp Asn Asp Phe Tyr Glu Met Arg Phe Ser His Gly Arg Leu Tyr Ala
    370                 375                 380
Ala Ser Gly Leu Trp Gly Thr Asn Leu Met Gly His Ala Gly Met Val
385                 390                 395                 400
Lys Leu Tyr Asp Gly Asn Arg Trp Thr Asn Phe Asp Lys Lys Thr Val
                405                 410                 415
Gln Glu Gln Leu Gly Gly Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile
            420                 425                 430
Ala Val Ser Asn Gly Asp Pro Asp His Phe Phe Val Gly Thr Trp Gly
        435                 440                 445
Asn Gly Leu Phe Glu Phe Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser
    450                 455                 460
Gly Asn Glu Thr Ala Ile Ala Glu Cys Asn Pro Gly Asp Ala Arg Val
465                 470                 475                 480
Lys Ala Ile Ala Phe Asp Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly
                485                 490                 495
Ala Val Gly Lys Asn Ile Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp
            500                 505                 510
His Ser Phe Ser Tyr Pro Asp Val Ala Asn Leu Ala Ser Phe Gly Asn
        515                 520                 525
Met Ile Ile Leu Pro Asn Gly Asp Lys Trp Val Asn Ile Leu His Arg
    530                 535                 540
Ser Gly Gly Ser Thr Arg Lys Gly Val Leu Ile Phe Asn Asp Arg Gly
545                 550                 555                 560
Thr Pro Glu Thr Thr Ser Asp Asp Ser His Leu Tyr Val Glu Gln Phe
                565                 570                 575
Val Asn Arg Leu Gly Ala Ala Ile Gly His Lys Thr Ile Tyr Ala Met
```

580 585 590

Ala Val Asp His Asn Gly Ser Val Trp Met Gly Ser Asp Ile Gly Ile

595 600 605

Phe Gly Val Tyr Asn Ala Ala Gly Val Leu Ser Ser Thr Ser Thr Pro

610 615 620

Ile Ala Val Arg Pro Val Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val

625 630 635 640

Leu Asp Lys Val Thr Val Thr Asp Ile Val Val Asp Lys Leu Asn His

645 650 655

Lys Trp Val Ala Thr Gln Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp

660 665 670

Cys Ser Lys Ile Leu Ala Gln Phe Thr Val Glu Asn Ser Pro Leu Leu

675 680 685

Ser Asn Asn Ile Leu Ser Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu

690 695 700

Tyr Ile Gly Thr Ala Asp Gly Leu Met Thr Phe Gln Thr Gly Thr Gly

705 710 715 720

Ser Gly Ser Ala Ser Glu Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro

725 730 735

Leu Arg Pro Glu Tyr Pro Asp Gly Val Thr Ile Ala Gly Leu Gln Ala

740 745 750

Gly Cys Ser Val Lys Ile Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln

755 760 765

Thr Glu Ser Val Thr Thr Glu Val Lys Trp Asn Ala Arg Gly Ala Asp

770 775 780

Gly Asn Arg Val Ala Ser Gly Val Tyr Ala Val Ala Val Tyr Asp Pro

785 790 795 800

Val Ser Lys Lys Ser Lys Leu Ile Arg Phe Ala Val Ile Arg

805 810

(2) INFORMATION FOR SEQ ID NO:88

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 451 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...451

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88

```
Lys Thr Ser Tyr Arg Asn Asn Met Arg Phe Gln His Tyr Leu Ile Cys
1               5                   10                  15
Thr Ala Ala Val Ala Ala Leu Ala Ala Asn Pro Leu Thr Gly Gln Ser
            20                  25                  30
Asn Met Thr Leu Glu Glu Cys Ile Asp Tyr Ala Arg Arg His Ser Ser
        35                  40                  45
Ala Val Ala Leu Ser Ala Ala Glu Leu Glu Gln Ser Lys Ala Asp Tyr
    50                  55                  60
Leu Gln Ala Val Gly Asn Phe Leu Pro Arg Val Ser Ala Gly Thr Gly
65                  70                  75                  80
Ala Ser Trp Asn Phe Gly Arg Gly Leu Asp Ala Glu Thr Asn Thr Tyr
                85                  90                  95
Thr Asp Ile Asn Ser Phe Asn Asn Ser Tyr Ser Ile His Ala Thr Met
            100                 105                 110
Thr Leu Phe Asp Gly Leu Gln Ser Val Tyr Arg Leu Arg Met Ala His
        115                 120                 125
Ala Arg Arg Glu Ala Ser Arg Leu Ser Val Arg Glu Gln Gln Glu Leu
    130                 135                 140
Ala Ala Leu Gly Thr Thr Glu Ala Tyr Tyr Asp Leu Val Tyr Ala Arg
145                 150                 155                 160
Gln Met Gln Glu Leu Ala Met Gln Lys Tyr Glu Glu Ser Ser Arg Leu
                165                 170                 175
```

```
His Arg Gln Thr Ala Arg Met Glu Glu Leu Gly Met Lys Ser Arg Pro
            180                 185                 190

Asp Val Leu Glu Met Gln Ser Arg Met Ala Gly Asp Arg Leu Ala Leu
        195                 200                 205

Thr Gln Ala Asp Asn Gln Cys Ile Ile Ala Leu Ile Arg Leu Lys Glu
    210                 215                 220

Lys Met Asn Phe Pro Ile Asp Asp Glu Leu Val Val Asp Asp Met Pro
225                 230                 235                 240

Ala Asp Ser Leu Ser Ala Asp Met Ala Glu Ser Asp Ser Ser Ala Gly
                245                 250                 255

Val Phe Ala Arg Ala Ala His His His Pro Val Leu Leu Arg Ala Lys
            260                 265                 270

Leu Asp Glu Gln Ala Ala Thr Asp Arg Leu Arg Ala Ala Arg Gly Ala
        275                 280                 285

Phe Leu Pro Ser Val Ser Val Ser Gly Gly Trp Asn Thr Gly Phe Ser
    290                 295                 300

Arg Phe Leu Asn Gly Ser Asp Tyr Thr Pro Phe Ser Glu Gln Phe Arg
305                 310                 315                 320

Asn Arg Arg Gly Glu Tyr Val Ser Leu Asn Leu Ser Ile Pro Ile Phe
                325                 330                 335

Ser Gly Phe Ser Leu Val Ser His Leu Arg Gln Ala Arg Ala Glu Arg
            340                 345                 350

Arg Ala Ala Ile Val Arg Arg Gly Glu Ala Glu Arg Arg Leu Tyr Ser
        355                 360                 365

Glu Ile Ala Gln Ala Met Ala Asp Arg Asp Ala Ala Leu Ala Ser Tyr
    370                 375                 380

Arg Gln Ala Lys Glu His Thr Asp Ala Met Gln Thr Ala Tyr Glu Ala
385                 390                 395                 400

Val Leu Gln Arg Tyr Glu Glu Gly Leu Asn Thr Ala Ile Asp Leu Thr
                405                 410                 415

Thr Gln Ala Asn Arg Leu Leu Asp Ala Arg Val Gln Arg Leu Arg Ala
            420                 425                 430

Ala Met Thr Tyr Arg Leu Lys Cys Lys Leu Ile Ala Tyr Tyr Gly Cys
        435                 440                 445

Leu Ser Asp
    450
```

(2) INFORMATION FOR SEQ ID NO:89

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 834 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89

```
Met Lys Arg Ile Val Leu Ser Ser Phe Leu Phe Val Leu Ser Ile Leu
1               5                   10                      15
Ser Leu Met Ala Gln Asn Asn Thr Leu Asp Val His Ile Ser Gly Thr
            20                  25                  30
Ile Lys Asp Ala Ser Ser Gly Glu Pro Val Pro Tyr Ala Thr Val Ser
        35                  40                  45
Ile Arg Leu Thr Gly Ala Asp Thr Thr Gln Val Phe Arg Gln Val Thr
    50                  55                  60
Asp Gly Asn Gly Tyr Phe Val Ile Gly Leu Pro Ala Ala Pro Ser Tyr
65                  70                  75                  80
His Leu Thr Ala Ser Phe Val Gly Met Lys Thr His Thr Met Gln Ile
                85                  90                  95
Ser Arg Gly Asn Gly Gln His Asp Ile Lys Ser Ile Asp Ile Ser Leu
            100                 105                 110
Glu Ser Glu Asp Lys Gln Leu Ser Thr Val Thr Val Ser Ala Ala Arg
```

```
        115                 120                 125
Pro Leu Val Lys Met Glu Ile Asp Arg Leu Ser Tyr Asn Met Lys Asp
    130                 135                 140
Asp Pro Ala Ala Lys Thr Asn Asn Leu Leu Glu Met Leu Arg Asn Val
145                 150                 155                 160
Pro Leu Val Thr Val Asp Gly Gln Gly Asn Ile Gln Val Lys Gly Ser
                165                 170                 175
Ser Asn Phe Lys Ile His Leu Asn Gly Arg Pro Ser Thr Met Val Ser
            180                 185                 190
Ser Asn Pro Lys Glu Val Phe Arg Ser Ile Pro Ala His Thr Ile Lys
        195                 200                 205
Arg Val Glu Val Ile Thr Asp Pro Gly Val Lys Tyr Asp Ala Glu Gly
    210                 215                 220
Thr Ser Ala Ile Leu Asp Ile Val Thr Glu Glu Gly Lys Lys Leu Glu
225                 230                 235                 240
Gly Tyr Ser Gly Ser Ile Thr Ala Ser Val Ser Asn Asn Pro Thr Ala
                245                 250                 255
Asn Gly Ser Ile Phe Leu Thr Ala Lys Ser Gly Lys Val Gly Leu Thr
            260                 265                 270
Thr Asn Tyr Asn Tyr Tyr Gly Gly Lys Asn Lys Gly Ser Arg Tyr Phe
        275                 280                 285
Thr Glu Arg Thr Thr Ser Met Leu Gln Thr Ile Glu Glu Gly Lys Gly
    290                 295                 300
Gln Glu Thr Phe Gly Gly His Phe Gly Asn Ala Leu Leu Ser Phe Glu
305                 310                 315                 320
Ile Asp Ser Leu Asn Leu Phe Thr Val Gly Gly Asn Val Arg Leu Trp
                325                 330                 335
Glu Met Thr Thr Asp Arg Asn Ser Val Glu Lys Ser Phe Ala Gly Ser
            340                 345                 350
Asn Leu Met Ser Tyr Ile Asp Arg Lys Leu Lys Thr Gln Met Asp Ala
        355                 360                 365
Gly Ser Tyr Glu Leu Asn Ala Asp Tyr Gln His Ser Thr Arg Leu Pro
    370                 375                 380
Gly Glu Leu Leu Thr Val Ser Tyr Arg Phe Thr His Asn Pro Asn Asn
385                 390                 395                 400
Ser Glu Thr Phe Ile Asp Gln Trp Lys Arg Asp Pro Leu Asn Thr Ala
```

```
                405                 410                 415
Asn Thr Ile Gln Tyr Ala Gly Gln His Ser Lys Ser Asp Ala Gly Met
            420                 425                 430
Asp Glu His Thr Ala Gln Val Asp Tyr Thr Arg Pro Leu Gly Gln Ala
        435                 440                 445
His Ser Leu Glu Ala Gly Leu Lys Tyr Ile Tyr Arg His Ala Thr Ser
    450                 455                 460
Asp Pro Leu Tyr Glu Ile Arg Pro Ser Glu Asp Ala Pro Trp Gln Pro
465                 470                 475                 480
Gly Ser Leu Tyr Ala Gln Asn Pro Ser Asn Gly Lys Phe Arg His Asp
                485                 490                 495
Gln Tyr Ile Gly Ala Ala Tyr Ala Gly Tyr Asn Tyr Arg Lys Asp Gln
            500                 505                 510
Tyr Ser Leu Gln Thr Gly Leu Arg Val Glu Ser Ser Arg Leu Lys Ala
        515                 520                 525
Leu Phe Pro Glu Asn Ala Ala Ala Asp Phe Ser His Asn Ser Phe Asp
    530                 535                 540
Trp Val Pro Gln Leu Thr Leu Gly Tyr Thr Pro Ser Pro Met Lys Gln
545                 550                 555                 560
Leu Lys Leu Ala Tyr Asn Phe Arg Ile Gln Arg Pro Ala Ile Gly Gln
                565                 570                 575
Leu Asn Pro Tyr Arg Leu Gln Thr Asn Asp Unk Gln Val Gln Tyr Gly
            580                 585                 590
Asn Pro Asp Leu Lys Ser Glu Lys Arg His His Val Gly Leu Ser Tyr
        595                 600                 605
Asn Gln Tyr Gly Ala Lys Val Met Leu Thr Ala Ser Leu Asp Tyr Asp
    610                 615                 620
Phe Cys Asn Asn Ala Ile Gln Asn Tyr Thr Phe Ser Asp Pro Ala Asn
625                 630                 635                 640
Pro Asn Leu Phe His Gln Thr Tyr Gly Asn Ile Gly Arg Glu His Ser
                645                 650                 655
Phe Ser Leu Asn Thr Tyr Ala Met Tyr Thr Pro Ala Val Trp Val Arg
            660                 665                 670
Ile Met Leu Asn Gly Asn Ile Asp Arg Thr Phe Gln Lys Ser Glu Ala
        675                 680                 685
Leu Gly Ile Asp Val Asn Ser Trp Ser Gly Met Val Tyr Ser Gly Leu
```

```
    690                 695                 700
Met Phe Thr Leu Pro Lys Asp Trp Thr Val Asn Leu Phe Gly Gly Tyr
705                 710                 715                 720
Tyr His Gly Gly Arg Ser Tyr Gln Thr Lys Tyr Asp Gly Asn Val Phe
                725                 730                 735
Asn Asn Ile Gly Ile Ala Lys Gln Leu Phe Asp Lys Lys Leu Arg Val
            740                 745                 750
Ser Leu Ser Ala Asn Asn Ile His Ala Lys Tyr Ser Thr Trp Lys Ser
        755                 760                 765
Arg Thr Ile Gly Asn Gly Phe Thr Ile Tyr Ser Glu Asn Ala Gly Ile
    770                 775                 780
Gln Arg Ser Val Ser Leu Ser Leu Thr Tyr Ser Phe Gly Lys Met Asn
785                 790                 795                 800
Thr Gln Val Arg Lys Val Glu Arg Thr Ile Val Asn Asp Asp Leu Lys
                805                 810                 815
Gln Thr Ser Ser Gln Gly Gln Gln Gly Gly Gly Gln Gly Asn Pro Thr
            820                 825                 830
Gly Asn
```

(2) INFORMATION FOR SEQ ID NO:90

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 593 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

```
Met Asn Ser Ile Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala
1               5                   10                  15
Leu Ser Val Ser Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr
            20                  25                  30
Lys Arg Pro Asp Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln
        35                  40                  45
Thr Val Glu Met Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala
    50                  55                  60
Ile Glu Pro Arg Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr
65                  70                  75                  80
Phe Gly Phe Val Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro
                85                  90                  95
Asn Ile Leu Pro Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn
            100                 105                 110
Ile Gly Ile Gly His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg
        115                 120                 125
Leu Ile Asp Ala Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg
    130                 135                 140
Gly Met Lys Ser Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys
145                 150                 155                 160
Asp Arg Arg Met Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser
                165                 170                 175
Phe Val Leu Ala Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn
            180                 185                 190
Tyr Gly Arg Gly Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser
        195                 200                 205
Thr Pro Val Thr Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val
    210                 215                 220
Tyr Leu Gly Ala Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg
225                 230                 235                 240
Phe Phe Arg Ser Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu
                245                 250                 255
```

```
Thr Glu His Thr Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser
            260                 265                 270
Asp Asp Ile Lys Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe
        275                 280                 285
Ala Lys Asn Ser Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp
    290                 295                 300
Arg Asn Leu Tyr Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly
305                 310                 315                 320
Asp Ser Asp Asn Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser
                325                 330                 335
Ser His Phe Gly Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp
            340                 345                 350
Ala Ser Leu Ser Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe
        355                 360                 365
Gly Gly Val Ile Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met
    370                 375                 380
Pro Tyr Leu Met Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu
385                 390                 395                 400
Thr Ala Gln Leu Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met
                405                 410                 415
Glu Val Tyr Gly Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr
            420                 425                 430
Pro Thr Leu Pro Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val
        435                 440                 445
Ser Phe Leu Pro Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly
    450                 455                 460
Lys Leu Glu Tyr Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala
465                 470                 475                 480
Ser Tyr Gly Lys Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln
                485                 490                 495
Pro Asp Leu Ile Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro
            500                 505                 510
Leu Asp Val Arg Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr
        515                 520                 525
Ser Phe Gly Ser Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His
    530                 535                 540
```

Leu Leu Ser Ala Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu

545 550 555 560

Tyr Leu Lys Ile Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly

565 570 575

Tyr Tyr Pro Met Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr

580 585 590

Phe

(2) INFORMATION FOR SEQ ID NO:91

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 589 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

Met Lys Tyr Gln Leu Tyr Thr Ala Val Ile Met Ala Leu Ser Val Ser

1 5 10 15

Ser Val Cys Gly Gln Thr Pro Arg Asn Thr Glu Thr Lys Arg Pro Asp

20 25 30

Thr Leu Arg Arg Glu Leu Thr Ile Val Asn Asp Gln Thr Val Glu Met

35 40 45

Glu His Ala Asp Pro Leu Pro Ala Ala Tyr Lys Ala Ile Glu Pro Arg

50 55 60

Leu Lys Pro Phe Arg Pro Glu Tyr Asn Lys Arg Thr Phe Gly Phe Val

65 70 75 80

Pro Glu Val Ser Ser Ser Gly Arg Asn Asn Leu Pro Asn Ile Leu Pro

85 90 95

Thr Glu Gly His Met Lys His Arg Gly Tyr Leu Asn Ile Gly Ile Gly

100 105 110

His Thr Leu Asn Gln Arg Met Asp Ala Gly Tyr Arg Leu Ile Asp Ala

115 120 125

Glu Gln Glu Arg Leu Asn Leu Phe Leu Ser Tyr Arg Gly Met Lys Ser

130 135 140

Ala Phe Asn Thr Gly Asp Phe Asp Gly Asp Arg Lys Asp Arg Arg Met

145 150 155 160

Met Ala Gly Val Asp Tyr Glu Gln Arg Arg Pro Ser Phe Val Leu Ala

165 170 175

Thr Gly Leu Tyr Tyr Ser Asn His Tyr Phe Asn Asn Tyr Gly Arg Gly

180 185 190

Ala Thr Thr Asn Val Gly Ser Ile Pro Gln Leu Ser Thr Pro Val Thr

195 200 205

Pro Gln Met Asp Asn Gly Thr His Asn Val Arg Val Tyr Leu Gly Ala

210 215 220

Lys Asn Asp Val Ile Asp Ala Arg Ile Asp Tyr Arg Phe Phe Arg Ser

225 230 235 240

Ile Pro Tyr Leu Gly Thr Asp Pro Met Lys Ala Leu Thr Glu His Thr

245 250 255

Pro Glu Leu Asn Val Thr Met Ser Asn Glu Leu Ser Asp Asp Ile Lys

260 265 270

Leu Gly Val Glu Val Arg Thr Gly Gly Leu Phe Phe Ala Lys Asn Ser

275 280 285

Glu Met Ile Gln Thr Gly Val Leu Ser Glu Thr Asp Arg Asn Leu Tyr

290 295 300

Tyr Val Glu Gly Ala Pro Thr Ile Gly Phe Val Gly Asp Ser Asp Asn

305 310 315 320

Met Gln Trp Asn Ile Gln Ala Gly Val Gly Ile Ser Ser His Phe Gly

325 330 335

Ala Lys Gly Arg Leu Phe Phe Trp Pro Lys Leu Asp Ala Ser Leu Ser

                340   345   350
Ile Phe Pro Ser Trp Arg Val Tyr Ala Lys Ala Phe Gly Gly Val Ile
            355   360   365
Arg Asn Gly Leu Ala Asp Val Met Gln Glu Glu Met Pro Tyr Leu Met
        370   375   380
Pro Asn Thr Ile Val Leu Pro Ser Arg Asn Ala Leu Thr Ala Gln Leu
385   390   395   400
Gly Val Lys Gly Asn Ile Ala Asp Val Val Arg Met Glu Val Tyr Gly
                405   410   415
Asp Phe Ser Lys Leu Thr Gly Val Pro Phe Tyr Thr Pro Thr Leu Pro
            420   425   430
Leu Tyr Asn Pro Ser Asp Leu Tyr Gln Tyr Asn Val Ser Phe Leu Pro
        435   440   445
Ile Tyr Ala Asp Gly Ser Arg Trp Arg Ala Gly Gly Lys Leu Glu Tyr
    450   455   460
Ser Tyr Arg Asp Met Leu Arg Phe Leu Val Asp Ala Ser Tyr Gly Lys
465   470   475   480
Trp Asn Leu Asp Gly Gly Leu Val Ala Ser Met Gln Pro Asp Leu Ile
                485   490   495
Leu Lys Ala Glu Val Gly Val His Pro Ile Ala Pro Leu Asp Val Arg
            500   505   510
Leu Arg Tyr Thr Gln Leu Asn Gly Arg Tyr Arg Tyr Ser Phe Gly Ser
        515   520   525
Ala Gly Ser Glu Ala Leu Gly Ile Gly Asn Val His Leu Leu Ser Ala
    530   535   540
Asp Val Ser Tyr Lys Leu Lys Lys Asn Leu Ser Leu Tyr Leu Lys Ile
545   550   555   560
Asp Asn Met Leu Ala Glu Thr Thr Glu Leu Ile Gly Tyr Tyr Pro Met
                565   570   575
Gln Pro Phe His Cys Phe Ala Gly Phe Ser Trp Thr Phe
            580   585

(2) INFORMATION FOR SEQ ID NO:92

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

```
Met Ile Arg Lys His Phe Gly Ile Ile Leu Gly Phe Leu Ser Leu Val
1               5                   10                  15
Phe Ser Ala Gly Ala Gln Gln Glu Lys Gln Val Phe His Phe Leu Asn
            20                  25                  30
Leu Pro Ala Thr Ala Gln Ala Leu Ala Ala Gly Gly Lys Ala Ile Thr
        35                  40                  45
Ile Val Asp Asp Asn Pro Gly Leu Ala Phe Glu Asn Pro Ala Leu Leu
    50                  55                  60
Gly Tyr Glu Ser Gly Gly Arg Ala Phe Leu Ser Tyr Leu Tyr Tyr Met
65                  70                  75                  80
Ser Gly Ser His Met Gly Asn Ala Cys Tyr Ala Ser Ser Val Gly Glu
                85                  90                  95
Arg Gly Met Trp Gly Val Gly Met Arg Phe Leu Asn Tyr Gly Ser Met
            100                 105                 110
Gln Gly Tyr Asp Gln Asn Ala Ile Ala Thr Gly Ser Phe Ser Ala Ser
        115                 120                 125
Asp Ile Ala Val Gln Gly Phe Tyr Ser His Glu Leu Ser Asn His Phe
    130                 135                 140
Arg Gly Gly Val Ser Leu Lys Ala Leu Tyr Ser Ser Ile Glu Thr Tyr
145                 150                 155                 160
```

```
Ser Ser Phe Gly Leu Gly Val Asp Val Gly Ile Ser Tyr Tyr Asp Asp
                165                 170                 175
Asp Lys Gly Tyr Ser Ala Ser Ala Leu Phe Lys Asn Val Gly Ala Gln
            180                 185                 190
Leu Lys Gly Tyr Asn Glu Glu Arg Glu Pro Leu Asp Trp Asp Phe Gln
        195                 200                 205
Leu Gly Phe Ser Arg Ser Phe Ile Asn Ala Pro Phe Arg Leu His Ile
    210                 215                 220
Thr Leu Phe Asn Leu Asn Pro His Tyr Phe Lys Arg Leu Val Pro Arg
225                 230                 235                 240
Asp Leu Ser Lys Met Gln Lys Phe Leu Arg His Phe Ser Ile Gly Ala
                245                 250                 255
Glu Phe Thr Pro Ser Glu Arg Phe Trp Val Gly Leu Gly Tyr Thr Pro
            260                 265                 270
Gln Ile Ala Gln Asp Phe Glu Val Glu Gly Gly Asn Lys Trp Gly Gly
        275                 280                 285
Leu Ser Ala Gly Val Gly Phe Thr Ser Gly Val Val Arg Val Gly Val
    290                 295                 300
Ser Ala Ala Thr Tyr His Pro Ala Ala Leu Ser Phe Met Cys Ser Val
305                 310                 315                 320
Gly Ile Arg Leu Asp Asp Lys Ser Ile Phe
                325                 330
```

(2) INFORMATION FOR SEQ ID NO:93

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

```
Met Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser
1               5                   10                  15
Ser Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr
            20                  25                  30
Phe Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro
        35                  40                  45
Val Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro
    50                  55                  60
Phe Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile
65                  70                  75                  80
Ala Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp
                85                  90                  95
Cys Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe
            100                 105                 110
Trp Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg
        115                 120                 125
Ile Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro
    130                 135                 140
Lys Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile
145                 150                 155                 160
Arg Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr
                165                 170                 175
Phe Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe
            180                 185                 190
Leu Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr
        195                 200                 205
Ala Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr
    210                 215                 220
Val Ser Gln Gln Lys
```

225

(2) INFORMATION FOR SEQ ID NO:94

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

```
Met Lys Lys Ala Phe Val Phe Val Leu Leu Val Cys Leu Phe Ser Ser
1               5                   10                  15
Phe Ser Ser Ser Ala Gln Thr Thr Thr Asn Ser Ser Arg Ser Tyr Phe
            20                  25                  30
Thr Gly Arg Ile Glu Lys Val Ser Leu Asn Leu Gly Val Pro Pro Val
        35                  40                  45
Ser Thr Glu Val Trp Gly Met Thr His Asp Ala Asn Gly Leu Pro Phe
    50                  55                  60
Glu Ile Pro Ile Ser Phe Ser Arg Phe Asn Ser Gln Gly Asp Ile Ala
65                  70                  75                  80
Thr Thr Tyr Tyr Ile Ala Asn Ser Glu Ala Thr Leu Asn Glu Trp Cys
                85                  90                  95
Asp Tyr Ala His Pro Gly Gly Ile Val Arg Val Glu Gly Arg Phe Trp
            100                 105                 110
```

```
Lys Met Thr Tyr Asn Ile Pro Thr Tyr Asn Ala Val Cys Thr Arg Ile
        115                 120                 125
Thr Phe Glu Asn Gln Glu Ile Glu Gly Thr Ile Val Leu Ile Pro Lys
    130                 135                 140
Pro Lys Val Ser Leu Pro His Val Ser Glu Ser Val Pro Cys Ile Arg
145                 150                 155                 160
Thr Glu Ala Gly Arg Glu Phe Ile Leu Cys Glu Glu Asp Asp Thr Phe
                165                 170                 175
Val Ser His Asp Gly Asn Glu Val Thr Ile Gly Gly Lys Pro Phe Leu
            180                 185                 190
Leu Asn Thr Asn Val Lys Ile Val Gly Asp Val Ser Gln Lys Tyr Ala
        195                 200                 205
Val Gly Val Gly Glu Ile Arg Phe Leu Gln Ile Cys Ala Gln Thr Val
    210                 215                 220
Ser Gln Gln Lys
225
```

(2) INFORMATION FOR SEQ ID NO:95

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 547 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

```
Met Lys Thr Ile Val Arg Tyr Ser Arg Leu Pro Val Ala Leu Phe Phe
1               5                   10                  15
Cys Leu Leu Gly Ala Val His Leu Ser Val Glu Ala Gln Met Leu Asn
            20                  25                  30
Thr Pro Phe Glu Leu Ser Asp Gln Ile Val Leu Ser Pro Thr Glu Arg
        35                  40                  45
Gln Tyr Arg Glu Ile Cys Val Gln Thr Lys Glu Lys Arg Gly Ala Asp
    50                  55                  60
Leu Phe Pro Leu Ser Asp Lys Leu Arg Asp Ser Ala Tyr Val Arg Phe
65                  70                  75                  80
Gly Ser Ala Tyr Gly Asp Ile Ala Gly Asp Tyr Leu Pro Tyr Asn Gly
                85                  90                  95
Asn Asn Tyr Ser Ser Leu Ser Leu Glu Ser Gly Gly Arg Ile Ser Val
            100                 105                 110
Arg Asn Tyr Gly Thr Leu Gln Gly Ser Ala Ser Tyr Ser Arg Gly Met
        115                 120                 125
His Lys Arg Ile Gly Trp Asn Ala Leu Arg Asn Ala Glu Ala Tyr Tyr
    130                 135                 140
Pro Tyr Leu Val Ser Asp Ser Thr Gly Gly Asp Tyr His Phe Glu Asp
145                 150                 155                 160
Tyr Arg Leu Ala Gly Tyr Tyr Ser Phe Arg Ala Gly Arg Leu Pro Leu
                165                 170                 175
Gly Ile Gly Phe Ser Tyr Arg Gly Glu Val Ala Tyr Arg Leu Thr Asp
            180                 185                 190
Pro Arg Thr Thr Asn Thr Thr Gly Ala Leu Glu Leu Ser Cys Ala Thr
        195                 200                 205
Ser Leu Thr Leu Pro Arg Glu Asn Arg Leu Ser Leu Ser Ala Ala Tyr
    210                 215                 220
Leu Tyr His Arg Gln His Leu Thr Gln Tyr Asn Trp Arg Pro Gly Gln
225                 230                 235                 240
Gln Asp Lys Phe Phe Val Ser Tyr Gly Phe Gly Gln Val Asp Val Ser
                245                 250                 255
Asn Ser Pro Ile Trp Phe Gly Ile Ser Arg Met Asn Tyr Val Asn Gly
            260                 265                 270
Trp Lys Leu Ser Ser Arg Leu Asp Thr Arg Arg Gly Asp Ala Ile Gly
```

```
        275                 280                 285
Leu Asp Tyr Ser Gly Tyr Phe Leu Asp Thr Glu Glu Arg Ser Ser Ile
    290                 295                 300
Asn Leu Phe Ala Leu Leu Tyr Asn Arg Leu Arg Leu Tyr Gly Ser Trp
305                 310                 315                 320
His Leu Ser Asp Phe Asp Phe Ser Phe Ser Ala Asp Tyr Ala Leu Arg
                325                 330                 335
Gln Gly Ile Glu Arg Ile Tyr Glu Asp Tyr Lys Pro Asp Asp Asn Tyr
            340                 345                 350
His Ile Tyr Asp Leu Arg Ile Leu Ala Ile Arg Arg Trp Tyr Met Leu
        355                 360                 365
Asn Glu Phe Ser Ala Gln Ala Gln Ala Ser Tyr Arg Ile Arg Thr Asp
    370                 375                 380
Arg Gly Cys Ala Leu Arg Val Ser Ala Gly Ser Asp Phe Tyr Gly Tyr
385                 390                 395                 400
Asp Glu Thr Tyr Arg Lys His Gly His His Thr Met Ser Gly Met Leu
                405                 410                 415
Arg Pro Phe Ala Gly Ile Ala Tyr Asp His Ala Gly Ser Lys Leu Asp
            420                 425                 430
Phe Gly Leu Ser Leu Ser Ala Ala Tyr Arg Met Val Leu Thr His Ser
        435                 440                 445
Tyr Lys Ile Arg Thr Ile Gln Lys Glu Gln Leu Asp Tyr Gln Leu Ala
    450                 455                 460
Tyr Leu Pro Tyr Ala Tyr Arg Asn Arg Glu Gly Val Glu Val Arg Ser
465                 470                 475                 480
Ser Leu Tyr Val Ser Ile Pro Met Gln Asn Thr His Arg Leu Met Thr
                485                 490                 495
Glu Leu Arg Leu Tyr Gly Asp Leu Met Lys Arg Lys Asp Gly Ile Ala
            500                 505                 510
Tyr Gly Lys Thr Pro Gly Val Ile Ser His Ile Leu Ser Asp Pro Gln
        515                 520                 525
Ala Glu Arg Thr Ser Gly His Thr Ile Gly Ala Ile Cys Asn Ile Ser
    530                 535                 540
Tyr Leu Phe
545
```

(2) INFORMATION FOR SEQ ID NO:96

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

```
Met Lys Lys Leu His Met Ile Ala Ala Leu Ala Val Leu Pro Phe Cys
1               5                   10                  15
Leu Thr Ala Gln Ala Pro Val Ser Asn Ser Glu Ile Asp Ser Leu Ser
            20                  25                  30
Asn Val Gln Leu Gln Thr Val Gln Val Val Ala Thr Arg Ala Thr Ala
        35                  40                  45
Lys Thr Pro Val Ala Tyr Thr Asn Val Arg Lys Ala Glu Leu Ser Lys
    50                  55                  60
Ser Asn Tyr Gly Arg Asp Ile Pro Tyr Leu Leu Met Leu Thr Pro Ser
65                  70                  75                  80
Val Val Ala Thr Ser Asp Ala Gly Thr Gly Ile Gly Tyr Ser Gly Phe
                85                  90                  95
Arg Val Arg Gly Thr Asp Ala Asn Arg Ile Asn Ile Thr Thr Asn Gly
            100                 105                 110
Val Pro Leu Asn Asp Ser Glu Ser Gln Ser Val Phe Trp Val Asn Met
        115                 120                 125
```

```
Pro Asp Phe Ala Ser Ser Ile Glu Asp Leu Gln Val Gln Arg Gly Val
    130                 135                 140
Gly Thr Ser Thr Asn Gly Ala Gly Ala Phe Gly Ala Ser Val Asn Met
145                 150                 155                 160
Arg Thr Asp Asn Leu Gly Leu Ala Pro Tyr Gly Arg Val Asp Leu Ser
                165                 170                 175
Gly Gly Ser Phe Gly Thr Phe Arg Arg Ser Val Lys Leu Gly Ser Gly
            180                 185                 190
Arg Ile Gly Arg His Trp Ala Val Asp Ala Arg Leu Ser Lys Ile Gly
        195                 200                 205
Ser Asp Gly Tyr Val Asp Arg Gly Ser Val Asp Leu Lys Ser Tyr Phe
    210                 215                 220
Ala Gln Val Gly Tyr Phe Gly Ser Asn Thr Ala Leu Arg Phe Ile Thr
225                 230                 235                 240
Phe Gly Gly Lys Glu Val Thr Gly Ile Ala Trp Asn Gly Leu Ser Lys
                245                 250                 255
Glu Asp Glu Ala Lys Tyr Gly Arg Arg Tyr Asn Ser Ala Gly Leu Met
            260                 265                 270
Tyr Val Asp Ala Gln Gly Val Pro His Tyr Tyr His Asn Thr Asp Asn
        275                 280                 285
Tyr Glu Gln Arg His Tyr His Ala Ile Met Thr His Ser Phe Ser Pro
    290                 295                 300
Ser Val Ile Leu Asn Leu Thr Ala His Tyr Thr Ala Gly Tyr Gly Tyr
305                 310                 315                 320
Thr Asp Glu Tyr Arg Thr Gly Arg Lys Leu Lys Glu Tyr Ala Leu Gln
                325                 330                 335
Pro Tyr Val Glu Asn Ser Val Thr Val Lys Lys Thr Asp Leu Ile Arg
            340                 345                 350
Gln Lys Tyr Leu Asp Asn Asp Phe Gly Gly Leu Ile Gly Ser Leu Asn
        355                 360                 365
Trp His Thr Gly Ala Trp Asp Leu Gln Phe Gly Ala Ser Gly Asn Ile
    370                 375                 380
Tyr Lys Gly Asp His Phe Gly Arg Ile Thr Tyr Ile Lys Lys Tyr Asn
385                 390                 395                 400
Gln Pro Leu Ala Pro Asp Phe Glu Tyr Tyr Arg Asn Arg Ala Asp Lys
                405                 410                 415
```

```
Arg Glu Gly Ala Ala Phe Ala Lys Ala Asn Trp Gln Ile Thr Pro Glu
            420                 425                 430
Leu Asn Met Tyr Ala Asp Leu Gln Tyr Arg Thr Ile Gly Tyr Thr Ile
        435                 440                 445
Asn Gly Ile Thr Asp Glu Tyr Asp Glu Val Gln Gly Ser Met Gln His
    450                 455                 460
Ile Asp Leu Asp Lys Thr Phe Arg Phe Leu Asn Pro Lys Ala Gly Leu
465                 470                 475                 480
Thr Tyr Ser Phe Asp Asp Ala His Thr Ala Tyr Ala Ser Val Ala Val
                485                 490                 495
Ala His Arg Glu Pro Asn Arg Thr Asn Tyr Thr Glu Ala Gly Ile Gly
            500                 505                 510
Gln Tyr Pro Thr Pro Glu Arg Leu Ile Asp Tyr Glu Leu Gly Tyr Arg
        515                 520                 525
Tyr Ala Ser Pro Leu Leu Ser Ala Gly Val Gly Leu Tyr Tyr Met Gln
    530                 535                 540
Tyr Lys Asp Gln Leu Val Leu Asp Gly Arg Leu Ser Asp Val Gly Gln
545                 550                 555                 560
Met Leu Thr Ser Asn Val Pro Asp Ser Tyr Arg Met Gly Leu Glu Leu
                565                 570                 575
Thr Leu Gly Trp Gln Ile Leu Pro Arg Leu Leu Arg Trp Asp Ala Ser
            580                 585                 590
Phe Thr Met Ser Arg Asn Lys Ile Asp Arg Tyr Val Gln Tyr Thr Ser
        595                 600                 605
Val Tyr Asp Ala Asp Tyr Asn Trp Leu Glu Leu Lys Glu Glu Thr Leu
    610                 615                 620
Glu Ser Thr Asp Ile Ala Tyr Ser Pro Asn Val Ile Ala Gly Ser Met
625                 630                 635                 640
Leu Thr Leu Ser His Ala Gly Phe Glu Met Ala Trp Thr Ser Arg Phe
                645                 650                 655
Val Ser Lys Gln Tyr Leu Asp Asn Thr Gln Arg Ser Asp Arg Met Leu
            660                 665                 670
Ser Ser Tyr Trp Val Asn Asp Leu Arg Leu Gly Tyr Val Leu Pro Val
        675                 680                 685
His Phe Val Lys Arg Val Ala Leu Gly Val Gln Leu Asn Asn Leu Phe
    690                 695                 700
```

```
Asn Leu Met Tyr Ala Ser Asn Ala Tyr Ile Tyr Asp Ala Gly Tyr Val
705                 710                 715                 720
Gln Ala Ser Gly Glu Leu Ser Ala Tyr Ala Asp Leu Arg Tyr Tyr Pro
                725                 730                 735
Gln Ala Gly Phe Asn Ala Leu Gly Unk Leu Thr Ile Asp Phe
            740                 745                 750
```

(2) INFORMATION FOR SEQ ID NO:97

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

```
Met Val Val Thr Leu Leu Val Ile Val Gly Ile Val Val Val Val Arg
1               5                   10                  15
Tyr Ser Leu Arg Val His Val His Lys Thr Gly Thr Val Val Ser Ala
            20                  25                  30
Ala Ile Phe Gly Phe Ile Leu Leu Gly Lys Thr Val Pro Cys Asp Thr
        35                  40                  45
Arg Asn Phe Phe Ser Ser Glu Ser Asp Glu Pro Glu Ser Arg Val Ala
    50                  55                  60
Thr Glu Ile Ala His Leu Cys Glu Ile Gly Phe Gln Ile His Ala Ser
```

```
65                  70                  75                  80
Ser Ile His Val Ala Val Arg Thr Asp Phe Gly Gln Ala Gly Ile His
                85                  90                  95
Cys Pro Met Ala Thr Asp Ala Ser Ala Thr Glu Phe Asp Arg Ser Ala
            100                 105                 110
Glu Cys Ala Glu Arg Thr Ser Ala Gln Ile Asp Thr Ala Ile Arg Ser
        115                 120                 125
Gln Ser Gln Ile Ile Arg Thr His Ile Asp Thr Cys Pro Lys Ser Ser
    130                 135                 140
Gly Thr Ile Gly Gly Ser Thr His Thr Ser Leu His Leu Lys Val Phe
145                 150                 155                 160
Asp Gly Arg Gly Glu Val Gly His Ile His Pro Lys Asp Gly Leu Arg
                165                 170                 175
Phe Gly Val Val Glu Gly Tyr Ser Ile Gly Ser Tyr Val Asp Ala Ile
            180                 185                 190
Gly Ile Gly Ala Thr His Ala Lys Ala Gly Ile Ser Asp Thr Arg Thr
        195                 200                 205
Gly Ile Ala Gly Gly Tyr His Gly Gly Ser Gln His Gln Gln Ile Gly
    210                 215                 220
Asp Val Thr Thr Ile Ile Gly Leu Gly Lys Phe Gly Leu Ala Asn Val
225                 230                 235                 240
Gly Val Ser Asp Arg Gly Phe Arg Arg Gly Ala Ser Ser Tyr Asp Leu
                245                 250                 255
Tyr Gly Leu Glu Leu His Ile Ala Lys Thr Ile Tyr Leu Ala Val Gly
            260                 265                 270
Asp Gly Cys Leu Cys Arg Gln Ala Glu Arg Gln Asp Gly
        275                 280                 285
```

(2) INFORMATION FOR SEQ ID NO:98

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

```
Met Lys Lys Ala Ile Leu Ser Gly Ala Ala Leu Leu Leu Gly Leu Cys
1               5                   10                  15
Ala Asn Ala Gln Asn Val Gln Leu His Tyr Asp Phe Gly His Ser Ile
            20                  25                  30
Tyr Asp Glu Leu Asp Gly Arg Pro Lys Leu Thr Thr Thr Val Glu Asn
        35                  40                  45
Phe Thr Pro Asp Lys Trp Gly Ser Thr Phe Phe Phe Ile Asp Met Asp
    50                  55                  60
Tyr Thr Gly Lys Gly Ile Gln Ser Ala Tyr Trp Glu Ile Ser Arg Glu
65                  70                  75                  80
Leu Lys Phe Trp Gln Ala Pro Val Ser Ile His Leu Glu Tyr Asn Gly
                85                  90                  95
Gly Leu Ser Thr Ser Phe Thr Phe Gly His Asp Ala Leu Ile Gly Ala
            100                 105                 110
Thr Tyr Thr Tyr Asn Asn Pro Ser Phe Thr Arg Gly Phe Thr Ile Thr
        115                 120                 125
Pro Met Tyr Lys His Leu Gly Ala His Asp Phe His Thr Tyr Gln Ile
    130                 135                 140
Thr Gly Thr Trp Tyr Met His Phe Leu Asp Gly Leu Leu Thr Phe Asn
145                 150                 155                 160
Gly Phe Leu Asp Leu Trp Gly Phe Pro Gln Glu Asn Pro Ile Gly Gly
                165                 170                 175
Pro Val Leu Lys Glu Gly Asp Lys Phe Val Phe Leu Ser Glu Pro Gln
            180                 185                 190
```

```
Phe Trp Ile Asn Leu Asn Arg Ile Lys Gly Ile Asp Lys Asp Phe Asn
        195                     200                     205
Leu Ser Ile Gly Thr Glu Met Glu Ile Ser Arg Asn Phe Ala Arg Met
    210                     215                     220
Asp Lys Phe Ser Cys Ile Pro Thr Leu Ala Val Lys Trp Thr Phe Asn
225                     230                     235                     240
```

(2) INFORMATION FOR SEQ ID NO:99

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 399 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

```
Met Arg Leu Ser Ala Ile Leu Ile Ala Leu Ile Val Met Leu Pro Ala
1               5                   10                  15
Val Leu Ser Gly Gln His Tyr Tyr Ser Met Ala Gly Glu Arg Leu Glu
            20                  25                  30
Thr Asp Ser Ile Arg Pro Asn Glu Leu Ser Ala Ser Ile Arg Ser Ala
        35                  40                  45
Leu Phe Phe Arg Asn Asn Glu Tyr Asn Ala Arg Ser Val Lys Gly Tyr
    50                  55                  60
Thr Leu Pro Gly Ala Arg Val Ser Ala Phe Ala Ser Tyr Ser Leu Pro
```

```
65                  70                  75                  80
Ala Ala His Gly Val Lys Leu Ser Leu Gly Val Ser Thr Leu Asn Tyr
                85                  90                  95
Trp Gly Ala Ser Arg Tyr Pro Ala Gly Ile Ala Tyr Ser Asp Leu Pro
            100                 105                 110
Tyr Trp Thr Asp Tyr Asn Asp Tyr Val Arg Leu Arg Ile Leu Pro Tyr
        115                 120                 125
Val Gln Ala Met Leu Lys Pro Thr Ala Thr Thr Ala Leu Met Leu Gly
    130                 135                 140
Asn Ile Ala Gly Gly Thr Ala His Gly Leu Ile Glu Pro Ile Tyr Asn
145                 150                 155                 160
Pro Glu Leu Asp Leu Thr Ala Asp Pro Glu Ala Gly Val Gln Phe Arg
                165                 170                 175
Gly Asp Trp Thr Arg Phe Arg Met Asp Val Trp Val Asn Trp Met Ser
            180                 185                 190
Met Ile Phe Lys Asn Asp Asn His Gln Glu Ser Phe Val Phe Gly Leu
        195                 200                 205
Ser Thr Thr Ser Lys Leu Leu Ser Gly Glu Gly Lys Trp Arg Leu Glu
    210                 215                 220
Leu Pro Leu Gln Ala Ile Ala Thr His Arg Gly Gly Glu Tyr Asn Trp
225                 230                 235                 240
Ala Gln Gln Asp Thr Val His Thr Trp Val Asn Gly Ala Val Gly Leu
                245                 250                 255
Lys Leu Ser Tyr Arg Pro Arg Thr Asp Lys Pro Met Gln Ile Trp Gly
            260                 265                 270
Ser Ala Tyr Gly Val Ala Ala Leu Ser Ser Gly Gly Tyr Phe Pro Tyr
        275                 280                 285
Glu Arg Gly Trp Gly Gly Tyr Leu Ser Leu Gly Met Asp Leu Glu His
    290                 295                 300
Phe Ala Phe Arg Thr Asp Tyr Trp Tyr Gly Arg His Tyr Val Ser Pro
305                 310                 315                 320
Phe Ala Ala Pro Phe Ala Asn Ser Leu Thr Tyr Asp Lys Gln Pro Leu
                325                 330                 335
Thr Asn Gly Trp Gly Asp Tyr Ile Arg Leu Tyr Ala Asp Tyr Ser Trp
            340                 345                 350
Arg Met Ala Arg Ser Val Ser Leu Ala Ala Val Ala Arg Val Trp Phe
```

```
        355                 360                 365
Gln Pro Ser Asp Arg Phe Ala Met Ser His Ala Leu Glu Leu Thr Met
    370                 375                 380
Arg Ile Asp Pro Lys Phe Pro Ile Ala Phe Leu Lys Gly Asn His
385                 390                 395
```

(2) INFORMATION FOR SEQ ID NO:100

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

```
Met Asn Lys Ser Leu Leu Ser Leu Ala Cys Leu Ile Leu Cys Gly Met
1               5                   10                  15
Pro Ala Ile Ala Gln Gln Thr Gly Pro Ala Glu Arg Ser Gly Glu Pro
            20                  25                  30
Ser Leu Ala Glu Arg Val Phe Gly Leu Glu Gln Lys Gln Lys Lys Leu
        35                  40                  45
Lys Val Tyr Leu Gly Ile Gln Ser Phe Tyr Asp Gln Pro Leu Val Asp
    50                  55                  60
Asp Glu Ser His Ile Gly His Phe Lys Val Gln Glu Leu Arg Met Ser
65                  70                  75                  80
```

```
Ala His Gly Glu Leu Asn Arg His Leu Ser Phe Asp Trp Arg Gln Arg
                85                  90                  95
Leu Asn Arg Ala Ala Asp Gly Thr Ser Phe Ala Asp Asn Leu Ser Asn
            100                 105                 110
Ala Ile Asp Ile Ala Gly Val Asp Trp His Pro Asn Asp Lys Val Ser
        115                 120                 125
Phe Phe Phe Gly Arg Gln Tyr Ala Arg Phe Gly Gly Ile Glu Tyr Asp
    130                 135                 140
Met Asn Pro Val Glu Ile Tyr Gln Tyr Ser Asp Leu Val Asp Tyr Met
145                 150                 155                 160
Thr Cys Tyr Thr Ser Gly Val Asn Phe Ala Trp Asn Phe His Pro Glu
                165                 170                 175
Gln Gln Leu Gln Leu Gln Val Leu Asn Ala Tyr Asn Asn Arg Phe Ala
            180                 185                 190
Asp Arg Tyr His Val Thr Pro Asp Val Ala Thr Ala Thr Ser Tyr Pro
        195                 200                 205
Leu Leu Tyr Ser Ala Gln Trp Asn Gly Thr Leu Leu Gly Gly Ala Leu
    210                 215                 220
His Met Arg Tyr Ala Val Ser Met Ala His Gln Ala Gln Glu Arg Asn
225                 230                 235                 240
Met Trp Tyr Phe Thr Ala Gly Asn Leu Phe Asn Pro Gly Lys Arg Ile
                245                 250                 255
Asn Gly Tyr Leu Asp Leu Thr Tyr Ser Ile Glu Gly Leu Asp Asp Lys
            260                 265                 270
Gly Ile Met Thr Ala Arg Tyr Gly Lys Gly Lys Thr Leu Thr Asp Val
        275                 280                 285
Lys Tyr Tyr Ala Leu Val Ser Lys Trp Asn Phe Arg Ile Phe Asp Gln
    290                 295                 300
Val Asn Leu Phe Leu Lys Gly Met Tyr Glu Asn Gly Tyr Ala Pro Ala
305                 310                 315                 320
Gln Tyr Gly Glu Ser Ser His Thr Arg His Ser Tyr Gly Tyr Met Gly
                325                 330                 335
Gly Val Glu Tyr Tyr Pro Thr Glu Thr Asn Phe Arg Leu Phe Val Thr
            340                 345                 350
Tyr Ile Gly Arg His Tyr Arg Tyr Ser Ala Thr Glu Thr Glu Ser Thr
        355                 360                 365
```

Asn Ala Leu Arg Ala Gly Leu Ile Tyr Gln Ile Pro Phe Leu
370 375 380

(2) INFORMATION FOR SEQ ID NO:101

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

Met Lys Arg Arg Phe Leu Ser Leu Leu Leu Leu Tyr Ile Leu Ser Ser
1 5 10 15
Ile Ser Leu Ser Ala Gln Arg Phe Pro Met Val Gln Gly Ile Glu Leu
20 25 30
Asp Thr Asp Ser Leu Phe Ser Leu Pro Lys Arg Pro Trp Arg Ala Ile
35 40 45
Gly Lys Thr Ile Gly Val Asn Leu Ala Val Trp Gly Phe Asp His Phe
50 55 60
Ile Met Asn Glu Asp Phe Ala Asp Ile Ser Trp Gln Thr Ile Lys Ser
65 70 75 80
Asn Phe Gln Thr Gly Phe Gly Trp Asp Asn Asp Lys Phe Val Thr Asn
85 90 95
Leu Phe Ala His Pro Tyr His Gly Ser Leu Tyr Phe Asn Ala Ala Arg

```
                100                     105                     110
Ser Asn Gly Leu Ser Phe Arg His Ser Ala Pro Phe Ala Phe Phe Gly
            115                     120                     125
Ser Leu Met Trp Glu Leu Leu Met Glu Asn Glu Pro Pro Ser Ile Asn
        130                     135                     140
Asp Leu Cys Ala Thr Thr Ile Gly Gly Ile Ala Leu Gly Glu Met Gly
145                     150                     155                     160
His Arg Leu Ser Asp Leu Leu Ile Asp Asn Arg Thr Thr Gly Trp Glu
                    165                     170                     175
Arg Met Gly Arg Glu Val Ala Ile Ala Leu Ile Asn Pro Met Arg Phe
                180                     185                     190
Leu Asn Arg Leu Thr Ala Gly Glu Val Thr Ser Val Gly Ser Arg Ser
            195                     200                     205
Gly Gln Ile Phe Gln Ser Val Pro Ile Asn Ile Val Val Asp Ala Gly
        210                     215                     220
Phe Arg Phe Leu Ala Asp Lys Arg His Ala Arg Thr Gly Ala Thr Ala
225                     230                     235                     240
Leu Thr Leu Asn Leu Arg Phe Asp Tyr Gly Asp Pro Phe Arg Ser Glu
                    245                     250                     255
Thr Phe Ser Pro Tyr Asp Phe Phe Gln Phe Lys Ala Gly Leu Ser Phe
                260                     265                     270
Ser Glu Ser Gln Pro Leu Leu Ser Gln Ile Asn Leu Ile Gly Ile Leu
            275                     280                     285
Ser Gly Cys Gln Leu Leu Ala His Glu Arg Thr Val Leu Val Gly Gly
        290                     295                     300
Leu Phe Gln His Phe Asp Tyr Tyr Asn Ser Glu Lys Arg Ile Ser Lys
305                     310                     315                     320
Asn Ser Glu Glu Val Leu Val Thr Pro Tyr Arg Ile Ser Gln Val Ala
                    325                     330                     335
Ala Leu Gly Gly Gly Leu Ile Phe Gln His His Gly Lys Phe Arg Arg
                340                     345                     350
Arg Pro Leu Glu Leu Tyr Ala Glu Thr Tyr Leu Asn Val Val Pro Met
            355                     360                     365
Gly Ala Ser Leu Ser Asp His Tyr Asn Val Asp Asn Arg Asp Tyr Asn
        370                     375                     380
Leu Gly Ser Gly Leu Ser Gly Lys Leu Tyr Leu Gly Ala Thr Tyr Asn
```

385 390 395 400

Asp Leu Trp Ser Trp Leu Leu Gly Val Glu Ser Tyr Arg Leu Tyr Thr

405 410 415

Trp Ile Gly Tyr Glu Glu Pro His Gln Lys Asn Thr Asp Val Ser Ser

420 425 430

Phe Met Val Gln Gly Asp Glu Ser Lys Ala Arg Leu Leu Val Thr Ser

435 440 445

Ser Glu Phe Ala Phe His Pro Gly Pro Trp His Val Ala Ile Val Ala

450 455 460

Arg Arg Phe Ile Arg Lys Thr Ala Tyr Gln Phe Tyr Pro Asn Val Ser

465 470 475 480

Phe Asp Thr Gly Asp Ile Gln Leu Arg Val Gly Phe His Phe

485 490

(2) INFORMATION FOR SEQ ID NO:102

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

Met Lys Arg Leu Ile Val Phe Leu Ala Met Gly Gly Leu Leu Phe Thr

1 5 10 15

```
Leu Ala Asn Ala Gln Glu Ala Asn Thr Ala Ser Asp Thr Pro Lys Lys
            20                  25                  30
Asp Trp Thr Ile Lys Gly Val Thr Gly Leu Asn Ala Ser Gln Thr Ser
        35                  40                  45
Leu Thr Asn Trp Ala Ala Gly Gly Glu Asn Thr Val Ala Gly Asn Leu
    50                  55                  60
Tyr Leu Asn Ile Asp Ala Asn Tyr Leu Lys Asp Lys Trp Ser Trp Asp
65                  70                  75                  80
Asn Gly Leu Arg Thr Asp Phe Gly Leu Thr Tyr Thr Thr Ala Asn Lys
                85                  90                  95
Trp Asn Lys Ser Val Asp Lys Ile Glu Leu Phe Thr Lys Ala Gly Tyr
            100                 105                 110
Glu Ile Gly Lys His Trp Tyr Gly Ser Ala Leu Phe Thr Phe Leu Ser
        115                 120                 125
Gln Tyr Ala Lys Gly Tyr Glu Lys Pro Ser Asp His Leu Thr Gly Val
    130                 135                 140
Lys His Ile Ser Asn Phe Phe Ala Pro Ala Tyr Leu Thr Leu Gly Ile
145                 150                 155                 160
Gly Ala Asp Tyr Lys Pro Asn Glu Lys Phe Ser Leu Tyr Leu Ser Pro
                165                 170                 175
Thr Thr Gly Lys Leu Thr Val Val Ala Asp Asp Tyr Leu Ser Ser Leu
            180                 185                 190
Gly Ala Phe Gly Val Lys Val Gly Glu Lys Thr Met Phe Glu Leu Gly
        195                 200                 205
Ala Leu Val Val Gly Ser Ala Asn Ile Asn Leu Met Glu Asn Val Asn
    210                 215                 220
Leu Ile Thr Lys Ala Ser Phe Phe Ser Ala Tyr Thr His Asp Phe Gly
225                 230                 235                 240
Asn Ile Asp Ile Asn Trp Glu Ala Met Leu Ala Met Lys Ile Asn Lys
                245                 250                 255
Phe Leu Thr Ala Thr Ile Ala Thr Asn Leu Ile Tyr Asp Asp Asp Val
            260                 265                 270
Lys Ile Asn Asp Gly Pro Lys Ile Gln Phe Lys Glu Val Val Gly Val
        275                 280                 285
Gly Val Ala Tyr Thr Phe
    290
```

(2) INFORMATION FOR SEQ ID NO:103

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 961 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

```
Met Lys Lys Leu Phe Pro Leu Leu Leu Leu Ile Leu Ser Ile Leu Val
1               5                   10                  15
Gly Cys Gly Lys Lys Glu Lys His Ser Val Thr Glu Ile Ala Unk Glu
            20                  25                  30
Lys Lys Arg Ile Thr Ala Leu Leu Tyr Glu Lys Glu Leu Pro Thr Asp
        35                  40                  45
Ser Val Lys Gln Leu Tyr Glu Asn Ser Val Gln Asn Lys Asn Leu Val
    50                  55                  60
Gly Gln Met Leu Phe Ala Ile Glu Val Gly Lys Arg Met Arg Asn Met
65                  70                  75                  80
Ser Gln Tyr Thr Asp Ala Met Leu Tyr His Gln Lys Gly Leu Asn Ala
                85                  90                  95
Ala Leu Asn Leu Arg Asp Thr Ile Val Ala Ala Gln Ala Trp Asn His
            100                 105                 110
Leu Gly Thr Asp Ser Arg Arg Ile Gly Ala Leu Ala Glu Ala Ser Asp
```

```
          115                 120                 125
Tyr His Tyr Lys Ala Leu Ser Leu Ile Glu Ser Phe Ser Gly Asn Gln
    130                 135                 140
Asn Arg Pro Ala Ile Lys Ala Arg Ser Ala Ala Leu Asn Gly Ile Gly
145                 150                 155                 160
Asn Ile Asn Leu Glu Leu Gly Tyr His Asp Glu Ala Glu Lys Asn Phe
                165                 170                 175
Leu Lys Ala Leu Gln Gly Glu Lys Glu Leu Asp Ser Pro Leu Gly Gln
            180                 185                 190
Ala Ile Asn Tyr Ala Asn Leu Gly Arg Ile Tyr Arg Gln Arg Lys Glu
        195                 200                 205
Tyr Asp Lys Ala Arg Thr Tyr Phe Leu Leu Ser Leu Glu Gln Asn Asn
    210                 215                 220
Met Ala Glu Asn Leu Met Gly Ile Gly Leu Cys Ser Ile Asn Leu Gly
225                 230                 235                 240
Glu Val Asp Glu Glu Lys Gly Asp Tyr Gln Lys Ala Leu Gln Glu Tyr
                245                 250                 255
Ala Thr Ala Tyr Lys Leu Met Glu Gln Leu Ser Asp Arg Trp His Trp
            260                 265                 270
Leu Asn Ser Cys Ile Pro Met Ala Arg Ile Asn Leu Lys Gln Gly Asn
        275                 280                 285
Glu Arg Leu Tyr Gln His Phe Ile Ser Leu Ala Glu Gly Thr Ala Lys
    290                 295                 300
Glu Ile Asn Ser Thr Ser His Leu Ile Glu Ile Tyr Asn Leu Gln Tyr
305                 310                 315                 320
Glu Asn Leu Glu Arg Lys Lys Glu Tyr Lys Gln Ala Leu Glu Ala Phe
                325                 330                 335
Cys Leu Ser Lys Thr Leu Ser Asp Ser Met Ser Ile Ala His Lys Val
            340                 345                 350
Ser Ser Ile Gln Glu Thr Arg Phe Asn Tyr Glu Arg Asn Lys Ser Gln
        355                 360                 365
Lys Glu Leu Glu Glu Ile Gln Gln Val Ser Lys Ala Lys Gln Glu Lys
    370                 375                 380
Ser Lys Phe Ile Leu Leu Ser Thr Leu Phe Ala Leu Phe Ile Ser Ile
385                 390                 395                 400
Leu Leu Ile Ser Val Leu Thr Tyr Ala Tyr Arg Gln Gly Lys Lys His
```

```
                405                 410                 415
Asn Lys Leu Ile Lys Glu Thr Asp Lys Leu Arg Ser Gly Phe Phe Thr
            420                 425                 430
Gly Ile Thr His Glu Phe Arg Thr Pro Ile Thr Val Ile Gln Gly Leu
        435                 440                 445
Asn Glu Lys Met Ser Ser Ser Pro Asp Leu Gln Ala Ser Asp Arg Thr
    450                 455                 460
Glu Leu His Lys Ile Ile Asp Arg Gln Ser Ser His Met Leu Asn Leu
465                 470                 475                 480
Val Asn Gln Leu Leu Asp Ile Cys Lys Ile Arg Ser Gly Val Ser Thr
                485                 490                 495
Pro Glu Trp Arg Asn Gly Asp Ile Val Ser Phe Val Gln Ile Leu Ile
            500                 505                 510
Asp Ser Phe Ala Pro Tyr Ala Gln Ala Gln Asp Ile Thr Leu Glu Leu
        515                 520                 525
Gln Pro Glu Ser Lys Pro Ile Val Val Asp Phe Val Pro Ser Tyr Leu
    530                 535                 540
Gln Lys Ile Ile Ser Asn Leu Leu Ser Asn Ala Ile Lys Tyr Ser Leu
545                 550                 555                 560
Ala Gly Gly Arg Val Val Ile Ser Leu Ala Lys Thr Lys Asn Glu Lys
                565                 570                 575
Asn Leu Ile Ile Arg Val Ala Asp Asn Gly Ile Gly Ile Asp Lys Thr
            580                 585                 590
Asp Gln Ala His Ile Phe Asp Ile Phe Tyr Arg Gly Gln Ser Ala Thr
        595                 600                 605
Glu Lys His Gly Ser Gly Val Gly Leu Ser Phe Thr Asn Ile Leu Val
    610                 615                 620
Glu Asn Leu Arg Gly Thr Ile Lys Val Glu Ser Gln Pro Gly Lys Gly
625                 630                 635                 640
Ser Ala Phe Thr Ile Ser Ile Pro Thr Gln Asn Gln Ser Ser Ser Ala
                645                 650                 655
Glu Ile Leu Pro Trp Leu Pro Ser Ser Asp Asp Ile Val Met Pro Val
            660                 665                 670
His Ile Ala Pro Asp Asp Ser Pro Thr Ser Pro Met Val Ala Ala Leu
        675                 680                 685
Asn His Arg Phe Glu Asp Glu Arg Pro Thr Ile Leu Leu Val Glu Asp
```

```
    690                 695                 700
Asn Lys Asp Ile Asn Leu Leu Val Lys Leu Leu Leu Cys Asp Arg Tyr
705                 710                 715                 720
Asn Val Leu Ser Ala Ala Asn Gly Lys Glu Gly Ile Ala Leu Ala Thr
                725                 730                 735
Glu His Ile Pro Asp Ile Ile Ile Thr Asp Ile Met Met Pro Ile Met
            740                 745                 750
Asp Gly Ile Glu Met Thr Ile Arg Met Lys Gln Ser Pro Leu Leu Cys
        755                 760                 765
His Ile Pro Ile Val Ala Leu Thr Ala Lys Ser Thr Glu Gln Asp Arg
    770                 775                 780
Leu Glu Gly Ile Lys Ser Gly Val Val Ser Tyr Leu Cys Lys Pro Phe
785                 790                 795                 800
Ser Pro Glu Glu Leu Leu Met Arg Ile Glu Gln Leu Leu Lys Asp Arg
                805                 810                 815
Glu Leu Leu Lys Lys Phe Tyr Met Gln Lys Leu Met Leu Asp Arg Lys
            820                 825                 830
Pro Glu Glu Glu Pro Gln Pro Ile Asp Asp Ser Ser Met Gln Phe Leu
        835                 840                 845
Leu Ala Ala Lys Asp Ala Val Ser Gly Gly Ile Lys Gln Asn Pro Asp
    850                 855                 860
Phe Ser Ala Gln Asp Leu Ala Glu Lys Met Cys Met Ser Pro Ser Gln
865                 870                 875                 880
Leu Asn Arg Lys Leu Thr Ser Val Val Gly Cys Ser Thr Ile Gly Tyr
                885                 890                 895
Ile Gln Gln Ile Lys Ile Lys Leu Ala Cys Lys Leu Leu Ala Asp Glu
            900                 905                 910
Ser Lys Asn Ile Ser Asp Ile Ser Ile Glu Ala Gly Phe Ser Asp Pro
        915                 920                 925
Ala Tyr Phe Ser Arg Thr Phe Lys Arg Tyr Met Asn Cys Ser Pro Ser
    930                 935                 940
Gln Tyr Arg Gln Lys Leu Leu Ala Met Pro Gly Ser Asp Lys Glu Thr
945                 950                 955                 960
Val
```

(2) INFORMATION FOR SEQ ID NO:104

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104

```
Met Lys His Leu Phe Lys Ser Thr Leu Val Leu Leu Cys Ala Leu Ser
1               5                   10                  15
Phe Ser Gly Thr Tyr Thr Phe Ala Gln Glu Asn Asn Thr Glu Lys Ser
            20                  25                  30
Arg Phe Asp Phe Ser Val Arg Leu Gly Gln Gly Tyr Ile Ala Gly Ser
        35                  40                  45
Thr Thr Asn Leu Met Tyr Gly Tyr Thr Ser Ala Asn Asp Arg Leu Leu
    50                  55                  60
Ser Gly Ala Ile Tyr Leu Gly Leu Thr Pro Ser Lys Lys Glu Asn Ala
65                  70                  75                  80
Thr Gly Val Ala Phe Arg Phe Leu Ser Pro Ser Pro Gly Tyr Tyr Val
                85                  90                  95
Asp Ile Ser Gly Lys Glu Asn Thr Leu Asn Tyr Ala Phe Tyr Val Val
            100                 105                 110
Gly Ala Tyr Asn Arg Ile Ala Ile Pro Ile Arg Pro Ile Lys Asn Phe
        115                 120                 125
```

```
Asn Phe Ile Phe Ser Thr Glu Val Gly Met Ala Trp Met Ser Arg His
    130                 135                 140
Glu Gln Ile Tyr Asn Ser Thr Ser Gln Thr Trp Asp Lys Gln Arg Lys
145                 150                 155                 160
Ser Arg Ser Gly Leu Asp Phe Gly Leu Gly Met His Leu Gln Unk His
                165                 170                 175
Ile Asn Lys Thr Val Tyr Phe Met Ala Gly Thr Asp Leu Thr Ser Cys
            180                 185                 190
Met Phe Gly Lys Arg Ile Asn Asp Tyr Gln Gln Lys Asp Arg Thr Phe
        195                 200                 205
Ile Ala Leu Ile Asp Asn Ser Ile Gly Ile Gly Leu Asn Leu
    210                 215                 220
```

(2) INFORMATION FOR SEQ ID NO:105

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1158 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105

```
Met Lys Arg Ile Leu Pro Ile Val Ala Phe Leu Ser Leu Phe Leu Ala
1               5                   10                  15
Leu Ala Leu Pro Ala Lys Ala Gln Arg Ala Met Gly Lys Thr Ala Asp
```

```
            20                  25                  30
Arg Ser Leu Met Ala Ser Gly His Trp Val Lys Ile Arg Val Asp Ala
        35                  40                  45
Ser Gly Val Tyr Arg Leu Thr Asp Glu Gln Leu Arg Ala Asn Gly Phe
    50                  55                  60
Ser Asp Pro Ser Lys Val Gly Val Phe Gly Tyr Gly Gly Gly Val Leu
65                  70                  75                  80
Pro Glu Asp Leu Ser Arg Ile Thr Thr Asp Asp Leu Pro Pro Val Pro
                85                  90                  95
Val Leu Arg Gln Gly Asn Ala Leu Tyr Phe Tyr Ala Val Gly Pro Val
            100                 105                 110
Thr Trp Phe Tyr Asn Pro Ala Lys Thr Thr Met Glu His Thr Val Asn
        115                 120                 125
Thr Tyr Ser Thr His Gly Tyr Tyr Phe Leu Ser Asp Ala Ala Gly Ala
    130                 135                 140
Pro Leu Gln Met Ser Gln Tyr Thr Gly Gly Gly Ala Ser Ala Glu Ala
145                 150                 155                 160
Leu Ile Asp Tyr Tyr Asp Glu Leu Met Leu His Glu Gln Glu Leu Tyr
                165                 170                 175
Ser Pro Lys Glu Ser Gly Arg Asp Leu Tyr Gly Glu Ser Phe Ser Ala
            180                 185                 190
Val Asn Thr Arg Thr Val Lys Phe Pro Leu Arg Gly Asn Thr Arg Ser
        195                 200                 205
Ser Gly Glu Leu Gly Thr Val Phe Ser Tyr Ile Ala Lys Ala Arg Ser
    210                 215                 220
Ala Gly Gly Gly Arg Glu Met Ser Leu Ser Ala Asn Gly Ile Leu Ile
225                 230                 235                 240
Phe Ser Asp Pro Phe Ser Met Thr Ser Asn Glu Val Ser Asn Ser Tyr
                245                 250                 255
Leu Ala Gly Lys Lys Arg Arg Leu Tyr His Ser Thr Pro Met Asn Ser
            260                 265                 270
Leu Val Asn Glu Leu Arg Leu Asp Ala Asn Tyr Ser Met Thr Gly Asp
        275                 280                 285
Ala Val Asn Leu Asp Phe Ile Glu Val Ala Thr Gln Asn Asp Leu Arg
    290                 295                 300
Tyr Asp Gly Ala Pro Met His Ile Arg Arg Phe Ser Asn Leu Pro Val
```

305 310 315 320

Leu Gly Gly Glu Ser Cys Arg Phe Val Ile Ser Glu Val Pro Glu Ser

325 330 335

Leu Val Val Leu Gln Ala Asn Ser Ser Leu Thr Ala Ser Leu Val Pro

340 345 350

Val Lys Thr Val Gly Asp Lys Thr Ile Glu Phe Val Ala Pro Pro Lys

355 360 365

Gly Gln Asp Arg Arg Thr Ile Asn Thr Phe Tyr Ala Val Asp Leu Ser

370 375 380

Gln Ala Ser Ala Pro Glu Ile Leu Gly Ala Val Pro Asn Gln Asn Leu

385 390 395 400

His Gly Glu Glu Ile Pro Asp Leu Ile Ile Val Ser Thr Gln Ala Leu

405 410 415

Leu Leu Glu Ala Asp Arg Leu Ala Thr Tyr Arg Arg Glu Lys Asn Gly

420 425 430

Leu Lys Val Leu Val Val Leu Gln Glu Gln Val Phe Asn Glu Phe Ser

435 440 445

Gly Gly Thr Pro Asp Ala Thr Ala Tyr Arg Leu Phe Ala Lys Met Phe

450 455 460

Tyr Asp Arg Trp Lys Ala Asn Ala Pro Val Gly Glu Thr Phe Pro Met

465 470 475 480

Gln Met Leu Leu Phe Gly Asp Gly Ala His Asp Asn Arg Lys Val Ser

485 490 495

Val Ala Trp Gln Lys Pro Tyr Leu Gln Gln Thr Glu Phe Leu Leu Thr

500 505 510

Phe Gln Ala Val Asn Ser Thr Asn Val Asn Ser Tyr Val Thr Asp Asp

515 520 525

Tyr Phe Gly Leu Leu Asp Asp Gln Pro Ala Ser Val Asn Ile Gly Trp

530 535 540

Arg Asn Tyr Asn Met Ala Val Gly Arg Phe Pro Val Arg Thr Pro Ala

545 550 555 560

Glu Ala Arg Ile Ala Val Asp Lys Thr Ile Arg Tyr Glu Glu Asp Arg

565 570 575

Glu Ser Gly Ala Trp Arg Ile Arg Ala Cys Phe Ala Ala Asp Asn Gly

580 585 590

Asp Lys His Ala Thr Glu Thr Ser Arg Leu Ile Asp Thr Val Lys Arg

```
        595                 600                 605
Tyr Ala Pro Ala Ile Met Pro Val Arg Ala Phe Gln Asp Val Tyr Pro
    610                 615                 620
His Val Ile Glu Asn Gly Leu His Ser Ile Pro Gly Ala Lys Lys Lys
625                 630                 635                 640
Met Leu Glu Thr Leu Gln Ser Gly Ile Ile Leu Leu Asn Tyr Ala Gly
                645                 650                 655
His Gly Gly Pro Ala Gly Trp Ser Asp Glu His Leu Leu Thr Leu Asn
            660                 665                 670
Asp Ile His Lys Phe Asn Tyr Lys His Met Pro Ile Trp Ile Thr Ala
        675                 680                 685
Thr Cys Asp Phe Ala Asn Tyr Asp Ser Gln Thr Thr Ser Ala Gly Glu
    690                 695                 700
Glu Val Phe Leu His Glu Lys Ser Gly Thr Pro Ile Met Phe Ser Thr
705                 710                 715                 720
Thr Arg Val Val Tyr Asn Thr Gln Asn Glu Lys Ile Asn Gly Phe Met
                725                 730                 735
Leu Arg Arg Met Phe Glu Lys Ala Lys Asp Gly Arg Tyr Arg Thr Met
            740                 745                 750
Gly Glu Ile Ile Arg Ser Ala Lys Gln Gly Met Leu Ser Thr Val Phe
        755                 760                 765
Pro Asp Ser Ile Asn Gln Leu Ser Phe Phe Leu Met Gly Asp Pro Ser
    770                 775                 780
Val Arg Met Asn Leu Pro Thr His Lys Val Gln Leu Thr Ala Ile Asn
785                 790                 795                 800
Gly Gln Asp Pro Glu Gly Gln Tyr Gly Thr Ile Met Leu Lys Ser Leu
                805                 810                 815
Glu Arg Val Ala Leu Lys Gly Lys Val Thr Asp Glu Lys Gly Thr Phe
            820                 825                 830
Asp Glu Thr Phe Ser Gly Lys Val Phe Leu Thr Val Phe Asp Gly Arg
        835                 840                 845
Lys Lys Met Thr Ala Leu Glu Glu Glu Gly Asn Asp Leu Ser Leu Val
    850                 855                 860
Tyr Tyr Asp Tyr Pro Asn Val Met Tyr Ala Gly Ile Ala Glu Val Lys
865                 870                 875                 880
Asp Gly Leu Phe Glu Thr Ser Phe Ile Val Pro Lys Asp Val Asn Tyr
```

```
                    885                 890                 895
Ser Glu His Glu Gly Arg Ile Asn Leu Tyr Ala Tyr Asn Glu Ser Thr
                900                 905                 910
Lys Ala Glu Ala Met Gly Val Asp Phe Ser Ile Arg Val Gln Pro Gly
            915                 920                 925
Ile Pro Asp Glu Val Thr Glu Asp Asn Thr Pro Pro Glu Ile Ile Ser
        930                 935                 940
Cys Phe Leu Asn Asp Ser Thr Phe Arg Ser Gly Asp Glu Val Asn Pro
945                 950                 955                 960
Thr Pro Leu Phe Met Ala Glu Val Phe Asp Leu Asn Gly Ile Asn Ile
                965                 970                 975
Thr Gly Ser Gly Val Gly His Asp Ile Thr Leu Cys Ile Asp Gly Arg
            980                 985                 990
Ala Asp Leu Thr Tyr Asn Leu Asn Ala Tyr Phe Thr Ser Ser Ala Thr
        995                 1000                1005
Asp Ala Gly Val Gly Thr Ile Leu Phe Met Ile Pro Ala Leu Ala Glu
    1010                1015                1020
Gly Asp His Thr Ala Arg Leu Thr Val Trp Asp Ile Phe Asn Asn Ala
1025                1030                1035                1040
Val His His Asp Phe Ser Phe Arg Val Val Asp Gly Ile Ala Pro Asp
                1045                1050                1055
Val Ala Asp Val Ile Leu Phe Pro Asn Pro Val Arg Glu Ser Ala Thr
            1060                1065                1070
Phe Arg Ile Phe His Asn Arg Pro Gly Ser Asp Leu Asn Val Ala Val
        1075                1080                1085
Glu Ile Tyr Asp Phe Thr Gly Arg Leu Val Asn Ser Leu Pro Val Lys
    1090                1095                1100
Thr Tyr Ser Ser Ser Tyr Gly Glu Pro Ile Glu Ile Lys Trp Asp Leu
1105                1110                1115                1120
Thr Ser Lys Tyr Gly Val Lys Ile Gly Asn Gly Phe Tyr Leu Tyr Arg
                1125                1130                1135
Cys Val Val Asn Ser Pro Gly Gly Gln Thr Ala Ser Met Ala Lys Lys
            1140                1145                1150
Met Ile Val Val Gly Gln
        1155
```

(2) INFORMATION FOR SEQ ID NO:106

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106

```
Met Ile Ile Lys Lys Met Leu Lys Asn Lys Leu Ala Pro Leu Ala Ile
1               5                   10                  15
Leu Phe Leu Phe Ala Pro Lys Ala Met Lys Ala Gln Glu Gln Leu Asn
            20                  25                  30
Val Val His Thr Ser Val Pro Ser Leu Asn Ile Ser Pro Asp Ala Arg
        35                  40                  45
Ala Ala Gly Met Gly Asp Ile Gly Val Ala Thr Thr Pro Asp Ala Tyr
    50                  55                  60
Ser Gln Tyr Trp Asn Pro Ser Lys Tyr Ala Phe Met Asp Thr Lys Ala
65                  70                  75                  80
Gly Ile Ser Phe Ser Tyr Thr Pro Trp Leu Ser Lys Leu Val Asn Asp
                85                  90                  95
Ile Ala Leu Met Gln Met Thr Gly Phe Tyr Lys Leu Gly Thr Asp Glu
            100                 105                 110
Asn Gln Ala Ile Ser Ala Ser Leu Arg Tyr Phe Thr Leu Gly Lys Leu
        115                 120                 125
```

```
Glu Thr Phe Asp Glu Leu Gly Glu Ser Met Gly Glu Ala His Pro Asn
    130                 135                 140
Glu Phe Ala Val Asp Leu Gly Tyr Ser Arg Gln Leu Ser Glu Asn Phe
145                 150                 155                 160
Ser Met Ala Val Ala Leu Arg Tyr Ile Arg Ser Asp Gln Ser Thr His
                165                 170                 175
Asn Thr Gly Glu Asn Gln Ala Gly Asn Ala Phe Ala Ala Asp Ile Ala
            180                 185                 190
Gly Tyr Leu Gln Lys Tyr Val Leu Leu Gly Asn Ala Glu Ser Leu Trp
        195                 200                 205
Ser Leu Gly Phe Asn Val Lys Asn Ile Gly Thr Lys Ile Ser Tyr Asp
    210                 215                 220
Gly Gly Val Thr Ser Phe Phe Ile Pro Thr Ser Leu Asn Leu Gly Thr
225                 230                 235                 240
Gly Leu Leu Tyr Pro Ile Asp Asp Tyr Asn Ser Ile Asn Phe Asn Leu
                245                 250                 255
Glu Leu Ser Lys Leu Leu Val Pro Thr Pro Pro Ile Met Asp Gln Asn
            260                 265                 270
Asp Gln Ala Gly Tyr Glu Ala Ala Leu Lys Lys Tyr Gln Glu Thr Ser
        275                 280                 285
Ser Ile Ser Gly Ile Phe Ser Ser Phe Gly Asp Ala Pro Gly Gly Leu
    290                 295                 300
Lys Glu Glu Phe Arg Glu Ile Thr Trp Gly Leu Gly Ala Glu Tyr Ser
305                 310                 315                 320
Tyr Asp Asp Lys Phe Phe Val Arg Ala Gly Tyr Ser Tyr Leu His Pro
                325                 330                 335
Thr Lys Gly Asn Leu Gln Tyr Phe Thr Ala Gly Ala Gly Phe Lys Met
            340                 345                 350
Asn Ile Phe Arg Ile Asp Ala Ser Tyr Leu Leu Ser Thr Ile Gln Ser
        355                 360                 365
Asn Pro Leu Asp Gln Thr Leu Arg Phe Thr Leu Ala Phe Asp Met Asp
    370                 375                 380
Gly Leu Arg Asn Leu Phe His
385                 390
```

(2) INFORMATION FOR SEQ ID NO:107

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107

Met Lys Lys Met Ile Leu Ala Ala Thr Met Leu Leu Ala Thr Ile Gly
1 5 10 15

Phe Ala Asn Ala Gln Ser Arg Pro Ala Leu Arg Leu Asp Ala Asn Phe
20 25 30

Val Gly Ser Asn Leu Met Gln Lys Val Ala Asn Thr Ser Val Asn Asn
35 40 45

Lys Met Ile Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Ala Leu
50 55 60

Ser Asn Asp Gly Phe Tyr Leu Ala Pro Gly Leu Ala Tyr Thr Met Arg
65 70 75 80

Gly Ala Lys Met Glu Ser Leu Ser Glu Thr Thr Thr Arg Leu His Tyr
85 90 95

Leu Gln Ile Pro Val Asn Ala Gly Met Arg Phe Ser Phe Ala Asp Asn
100 105 110

Met Ala Ile Ser Leu Glu Ala Gly Pro Tyr Phe Ala Tyr Gly Val Ala
115 120 125

Gly Thr Ile Lys Thr Lys Val Ala Gly Val Thr Ala Ser Val Asp Ala

```
    130                 135                 140
Phe Gly Asp Asn Gly Tyr Asn Arg Phe Asp Leu Gly Leu Gly Leu Ser
145                 150                 155                 160
Ala Ala Leu Ser Tyr Asp Arg Tyr Tyr Val Gln Ile Gly Tyr Glu His
                165                 170                 175
Gly Leu Leu Asn Met Leu Lys Asp Ala Pro Asp Lys Thr Ser Leu Arg
            180                 185                 190
Asn His Asp Phe Phe Val Gly Leu Gly Val Arg Phe
        195                 200
```

(2) INFORMATION FOR SEQ ID NO:108

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 455 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

```
Met Lys Arg Thr Ile Leu Leu Thr Ala Leu Thr Val Leu Ser Ser Leu
1               5                   10                  15
Ser Leu Leu Arg Ala Gln Asn Glu Ser Glu Ala Ser Thr Asn Pro Met
            20                  25                  30
Ser Gly Leu Ser Leu Glu Asp Cys Ile Arg Ile Ala Lys Glu Arg Asn
        35                  40                  45
```

```
Leu Asn Leu Arg Arg Gln Glu Ile Glu Gln Glu Asn Arg Ile Ile Ser
    50                  55                  60
Leu Asp Ala Ala Arg His Ser Phe Leu Pro Ser Val Asn Ala Gly Ile
65                  70                  75                  80
Gly His Asn Tyr Ser Phe Gly Arg Ser Lys Asp Lys Thr Gly Val Thr
                85                  90                  95
Val Asp Arg Ser Ser Met Asn Thr Asn Leu Ser Ile Gly Ala Ser Val
            100                 105                 110
Glu Val Phe Ser Gly Thr Arg Arg Leu His Asp Leu Lys Gln Gln Lys
        115                 120                 125
Tyr Asn Val Glu Asp Gly Ile Ala Arg Leu Gln Lys Ala Arg Glu Asp
    130                 135                 140
Leu Ser Leu Gln Ile Ala Ala Leu Tyr Ile Asn Leu Leu Phe Arg Gln
145                 150                 155                 160
Glu Met Thr Arg Thr Ala Glu Thr Gln Leu Ala Leu Ile Arg Glu Gln
                165                 170                 175
Arg Asn Arg Thr Ala Glu Met Val Arg Val Gly Lys Trp Ala Glu Gly
            180                 185                 190
Lys Leu Leu Asp Ile Asn Ala Gln Met Ala Lys Asp Glu Gln Leu Leu
        195                 200                 205
Val Gln Tyr Arg Ser Glu Glu Glu Leu Ala Arg Leu Asp Leu Gly Gln
    210                 215                 220
Ala Leu Glu Leu Glu His Pro Glu Ser Ile Ala Val Lys Ala Pro Asp
225                 230                 235                 240
Thr Asp Val Leu Val Ala Glu Arg Leu Gly Ser Leu Leu Ala Pro Glu
                245                 250                 255
Glu Ile Tyr Arg Thr Ala Leu Gly Leu Lys Pro Ala Leu His Ser Ser
            260                 265                 270
Glu Leu Gln Ile Ala Ser Ala Arg Glu Gly Leu Ala Ser Ala Arg Ala
        275                 280                 285
Ala Tyr Phe Pro Thr Leu Ser Leu Ser Ala Gly Tyr Ser Asn Gly Tyr
    290                 295                 300
Phe Arg Asp Leu Gly Lys Glu Tyr Ala Ala Ile Asn Pro Ser Phe Ser
305                 310                 315                 320
Glu Gln Trp Lys Asn Asn Gly Ser Tyr Ser Ile Gly Leu Ser Leu Asn
                325                 330                 335
```

```
Ile Pro Ile Phe Ser Ala Met Gln Thr Gln Asp Arg Val Arg Ser Ser
            340                 345                 350
Arg Leu Gln Ile Arg Ser Ser Glu Leu Arg Leu Val Glu Glu Lys Lys
        355                 360                 365
Ala Leu Tyr Lys Glu Ile Arg Gln Ala Tyr Ser Asn Ala Val Ala Ala
    370                 375                 380
Asp Lys Ala Ile Ala Ala Ala Glu Asn Ser Lys Ala Ala Thr Leu Lys
385                 390                 395                 400
Ala Tyr Glu Tyr Ala Arg Asp Ser Phe Glu Ala Gly Arg Leu Ser Ala
                405                 410                 415
Tyr Glu Tyr Ala Glu Ala Lys Thr Lys Tyr Ala Leu Ser Gln Val Glu
            420                 425                 430
Glu Leu Arg Ala Lys Tyr Asp Phe Ile Tyr Lys Ala Lys Val Leu Asp
        435                 440                 445
Phe Tyr Gln Gly Lys Asp Phe
    450                 455
```

(2) INFORMATION FOR SEQ ID NO:109

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 434 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109

```
Met Tyr Lys Asp Tyr Lys Gly Leu Tyr Ala Ser Leu Arg Trp Tyr Ala
1               5                   10                  15
Leu Ile Ile Gly Leu Leu Phe Ala Ala Asp Gly Ile Gln Ala Gln Asn
            20                  25                  30
Asn Asn Phe Thr Glu Ser Pro Tyr Thr Arg Phe Gly Leu Gly Arg Leu
        35                  40                  45
Gly Glu Arg Thr Thr Ile Ser Gly His Ser Met Gly Gly Leu Gly Val
    50                  55                  60
Gly Leu Arg Gln Gly Thr Tyr Val Asn Ala Val Asn Pro Ala Ser Tyr
65                  70                  75                  80
Ser Ala Val Asp Ser Met Thr Phe Ile Phe Asp Phe Gly Ala Ser Thr
                85                  90                  95
Gly Ile Thr Trp Tyr Ala Glu Asn Gly Lys Lys Asp Asn Arg Lys Met
            100                 105                 110
Gly Asn Ile Glu Tyr Phe Ala Met Leu Phe Pro Ile Ser Lys Ser Ile
        115                 120                 125
Ala Met Ser Ala Gly Val Leu Pro Tyr Ser Ala Ser Gly Tyr Gln Phe
    130                 135                 140
Gly Ser Val Asp Gln Val Glu Gly Gly Ser Val Gln Tyr Thr Arg Lys
145                 150                 155                 160
Tyr Leu Gly Thr Gly Asn Leu Asn Asp Leu Tyr Val Gly Ile Gly Ala
                165                 170                 175
Thr Pro Phe Lys Asn Phe Ser Ile Gly Ala Asn Ala Ser Ser Leu Phe
            180                 185                 190
Gly Arg Phe Thr His Ser Arg Gln Val Ile Phe Ser Thr Glu Ala Pro
        195                 200                 205
Tyr Asn Pro Val His Leu Ser Thr Leu Tyr Leu Lys Ala Ala Lys Phe
    210                 215                 220
Asp Phe Gly Met Gln Tyr His Leu Leu Leu Lys Ser Asp Arg Ser Leu
225                 230                 235                 240
Val Ile Gly Ala Val Tyr Ser Pro Arg Val Lys Met His Ser Glu Leu
                245                 250                 255
Thr Gln Ile Lys Asn Gln Val Gln Asn Gly Val Val Val Glu Ser Glu
            260                 265                 270
Thr Gln Glu Tyr Ile Lys Gly Met Asp Tyr Tyr Thr Leu Pro His Thr
```

```
        275                 280                 285
Leu Gly Ile Gly Phe Ser Tyr Glu Lys Lys Asp Lys Leu Leu Leu Gly
    290                 295                 300
Ala Asp Val Gln Tyr Ser Lys Trp Lys Gly Glu Lys Phe Tyr Lys Ser
305                 310                 315                 320
Asp Cys Lys Phe Gln Asp Arg Ile Arg Val Ser Leu Gly Gly Glu Ile
                325                 330                 335
Ile Pro Asp Ile Asn Ala Val Gly Met Trp Pro Lys Val Arg Tyr Arg
            340                 345                 350
Phe Gly Leu His Gly Glu Asn Ser Tyr Leu Lys Val Pro Thr Lys Gly
        355                 360                 365
Gly Val Tyr Gln Gly Tyr His Ile Val Gly Ala Val Phe Gly Ile Gly
    370                 375                 380
Ile Pro Leu Asn Asp Arg Arg Ser Phe Val Asn Val Ser Leu Glu Tyr
385                 390                 395                 400
Asp Arg Leu Ile Pro Lys Glu Gly Met Ile Lys Glu Asn Ala Leu Lys
                405                 410                 415
Leu Thr Phe Gly Leu Thr Phe Asn Glu Ser Trp Phe Lys Lys Leu Lys
            420                 425                 430
Leu Asn
```

(2) INFORMATION FOR SEQ ID NO:110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110

```
Met Arg Ser Ile Tyr Gln Leu Leu Leu Ser Ile Leu Leu Ala Ser Leu
1               5                   10                  15
Gly Phe Val Gly Leu Glu Ala Gln Gln Ala Gly Val Ala Gly Arg Val
            20                  25                  30
Leu Asp Glu Glu Gly Asn Pro Met Ile Gln Ala Asn Val Gln Leu Val
        35                  40                  45
Gln Ser Thr Gly Gln Val Ala Val Ala Ala Gly Ala Thr Asn Glu Lys
    50                  55                  60
Gly Leu Phe Ser Leu Lys Thr Ser Gln Glu Gly Asp Tyr Ile Leu Arg
65                  70                  75                  80
Val Ser Tyr Val Gly Tyr Thr Thr His Asp Glu Lys Ile Ser Leu Arg
                85                  90                  95
Asn Gly Gln Thr Ile Thr Leu Lys Asp Ile Ser Met Asn Glu Asp Ala
            100                 105                 110
Arg Leu Leu Gln Ser Val Thr Val Gln Ala Lys Ala Ala Glu Val Val
        115                 120                 125
Val Arg Asn Asp Thr Leu Glu Phe Asn Ala Gly Ser Tyr Thr Val Ala
    130                 135                 140
Gln Gly Ala Ser Ile Glu Glu Leu Ile Lys Lys Leu Pro Gly Ala Glu
145                 150                 155                 160
Ile Gly Ser Asp Gly Lys Ile Thr Ile Asn Gly Lys Asp Ile Ser Lys
                165                 170                 175
Ile Leu Val Asp Gly Lys Glu Phe Phe Ser Lys Asp Pro Gln Val Ala
            180                 185                 190
Ile Lys Asn Leu Pro Ala Asp Met Val Asn Lys Val Gln Val Leu Asn
        195                 200                 205
Lys Leu Ser Glu Leu Ser Arg Met Ser Gly Phe Asp Asp Gly Glu Glu
    210                 215                 220
Glu Thr Val Ile Asn Leu Thr Val Lys Pro Glu Lys Lys Lys Gly Leu
225                 230                 235                 240
```

```
Phe Gly Thr Leu Gln Ala Gly Tyr Gly Thr Asp Gln Arg Tyr Met Ala
                245                 250                 255
Gly Gly Asn Val Asn Arg Phe Asp Gly Asn Lys Gln Trp Thr Leu Ile
            260                 265                 270
Gly Ser Ala Asn Asn Thr Asn Asn Met Gly Phe Ser Glu Met Asp Ser
        275                 280                 285
Glu Met Gly Ser Met Thr Phe Phe Ser Pro Gln Gly Gly Gly Arg Arg
    290                 295                 300
Gly Phe Gly Asn Ser Gly Gly Val Thr Ser Ser Ser Met Leu Gly Gly
305                 310                 315                 320
Asn Phe Ser Val Glu Phe Ser Ser Ala Leu Asn Thr Gly Gly Asp Ala
                325                 330                 335
Arg Tyr Gly Tyr Asn Asp Lys Ala Ile Glu Thr Thr Lys Arg Val Glu
            340                 345                 350
Asn Ile Leu Ala Glu Gly Asn Thr Tyr Met Asp Glu Asn Ile Leu Glu
        355                 360                 365
Arg Ser Phe Ser His Asn Gly Gln Ala Arg Phe Arg Met Gln Trp Lys
    370                 375                 380
Pro Ser Glu Arg Thr Glu Val Val Phe Glu Pro Asp Leu Ser Ile Ser
385                 390                 395                 400
Lys Ile Asp Gly Phe Phe Asn Asp Thr Tyr Glu Thr Lys Asp Ala Thr
                405                 410                 415
Gly Ile Ser Ile Asn Lys Gly Ser Ile His Gln Thr Thr Gln Gly Asn
            420                 425                 430
Asn Phe Arg Leu Asn Gly Glu Leu Asp Ile Ser His Lys Leu Asn Asp
        435                 440                 445
Glu Gly Arg Thr Ile Ser Ala Ser Val Ser Gly Gly Leu Thr Asp Glu
    450                 455                 460
Asp Gly Asp Gly Ile Tyr Gln Ala Val Leu Gln Ser Val Glu Thr Asn
465                 470                 475                 480
Gln Lys Gln Phe Asn Asp Asn Ser Asn Leu Gln Tyr Arg Leu Arg Leu
                485                 490                 495
Ser Tyr Val Glu Pro Leu Gly Lys Asn Tyr Phe Ala Gln Ala Ile Leu
            500                 505                 510
Asn Arg Arg Phe Ser Arg Arg Asn Ser Asp Arg Glu Val Tyr Arg Leu
        515                 520                 525
```

```
Gly Asp Asp Gly Gln Tyr Ser Ile Leu Asp Ser Gln Tyr Gly Leu Ser
    530                 535                 540
Tyr Ser Asn Glu Phe Thr Gln Tyr Arg Ile Gly Leu Asn Leu Lys Lys
545                 550                 555                 560
Ile Ala Lys Thr Trp Asp Tyr Thr Val Gly Phe Asn Val Asp Pro Asn
                565                 570                 575
Arg Thr Val Ser Tyr Arg Ser Val Ala Gly Val Glu Gln Asp Lys Leu
            580                 585                 590
Ala Phe Asn Arg Val Asn Leu Ser Pro Met Leu Arg Ile Asn Tyr Lys
        595                 600                 605
Pro Ser Arg Thr Thr Asn Leu Arg Val Asp Tyr Arg Gly Arg Thr Thr
    610                 615                 620
Gln Pro Ser Ile Asn Gln Ile Ala Pro Val Gln Asp Ile Thr Asn Pro
625                 630                 635                 640
Leu Phe Val Thr Glu Gly Asn Pro Gly Leu Lys Pro Ser Tyr Ser Asn
                645                 650                 655
Asn Val Met Ala Met Phe Ser Asp Phe Asp Ala Lys Ser Gln Arg Ala
            660                 665                 670
Phe Asn Ile Val Phe Phe Gly Asn Tyr Thr Phe Asp Asp Ile Val Pro
        675                 680                 685
Asn Thr His Tyr Asp Pro Ser Thr Gly Ile Arg Thr Thr Arg Tyr Glu
    690                 695                 700
Asn Ala Ser Gly Thr Trp Gln Ala Asn Leu His Gly Thr Leu Ser Leu
705                 710                 715                 720
Pro Leu Lys Asn Arg Ala Phe Ser Phe Arg Met Ser Leu Phe Asn Arg
                725                 730                 735
Leu Ala Glu Gly Gln Ser Phe Ile Asn Asp Asp Lys Asn Lys Ala Leu
            740                 745                 750
Ser Phe Arg Thr Arg Glu Arg Leu Thr Leu Thr Tyr Arg Asn Asn Trp
        755                 760                 765
Ile Asp Thr Ser Ile Gly Gly Asn Ile Gly Phe Tyr Met Ala Asn Asn
    770                 775                 780
Ser Leu Ser Gly Gln Lys Asp Ser Arg Thr Tyr Asp Phe Gly Gly Asn
785                 790                 795                 800
Tyr Gln Val Ala Leu Thr Leu Pro Tyr Gly Phe Arg Ile Asp Ser Asp
                805                 810                 815
```

Val Glu Tyr Asn Thr Asn Ser Gly Tyr Ser Gly Gly Phe Ser Leu Asp
820 825 830

Glu Trp Leu Trp Asn Ala Ser Leu Ser Tyr Ser Phe Leu Arg Asp Lys
835 840 845

Ala Gly Thr Leu Arg Val Asn Gly Tyr Asp Ile Leu Gly Gln Arg Ser
850 855 860

Ser Ile Ser Arg Ser Ala Ser Ala Ile Asn Ile Glu Glu Ser Met Ser
865 870 875 880

Asn Thr Ile Gly Arg Tyr Val Met Val Asp Phe Ile Tyr Arg Phe Asn
885 890 895

Ala Phe Ser Gly Gly Gly Ser Arg Ser Asp His Gln Arg Gly Asn Met
900 905 910

Asn Arg Pro Gly Pro Pro Phe Gly Gly Gly Arg Arg Pro Ser
915 920 925

(2) INFORMATION FOR SEQ ID NO:111

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 781 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111

Met Asp Arg Pro Lys Pro Ser Tyr Ile Val Arg Ile Ala Ala Ile Leu

```
1               5                   10                  15
Cys Leu Phe Val Gly Arg Pro Leu Phe Ala Gln Ser Tyr Val Asp Tyr
            20                  25                  30
Val Asp Pro Leu Ile Gly Thr Leu Ser Ser Phe Glu Leu Ser Ala Gly
        35                  40                  45
Asn Thr Tyr Pro Val Ile Gly Leu Pro Trp Gly Met Asn Ser Trp Thr
    50                  55                  60
Pro Met Thr Gly Val Pro Gly Asp Gly Trp Gln Tyr Thr Tyr Ser Ala
65                  70                  75                  80
His Lys Ile Arg Gly Phe Lys Gln Thr His Gln Pro Ser Pro Trp Ile
                85                  90                  95
Asn Asp Tyr Gly Gln Phe Ser Leu Leu Pro Leu Thr Ala Pro Gln Lys
            100                 105                 110
Pro Ser Ser Asn Asp Ser Ile Ala Leu Thr Lys Trp Cys Lys Gln Leu
        115                 120                 125
Phe Ser Asp Glu Gln Thr Ser Trp Phe Ser His Lys Ala Glu Thr Ala
    130                 135                 140
Thr Pro Tyr Tyr Tyr Ser Val Tyr Leu Ala Asp Tyr Asp Thr Arg Val
145                 150                 155                 160
Glu Met Ala Pro Thr Glu Arg Ala Ala Ile Phe Arg Ile Arg Tyr Ser
                165                 170                 175
Gly Asn Thr Glu Ser Gly Ser Gly Arg Trp Leu Arg Leu Asp Ala Phe
            180                 185                 190
Thr Gly Gly Ser Glu Ile Ser Ile Val Asp Pro His Thr Val Val Gly
        195                 200                 205
Ile Ser Arg Lys Asn Ser Gly Gly Val Pro Ala Asn Phe Ala Cys Tyr
    210                 215                 220
Phe Ile Leu Gln Ser Asp Thr Pro Met Ala Asp Val Leu Leu Glu Thr
225                 230                 235                 240
Asp Thr Gly Lys Ser Asp Glu Gly Thr Arg Ala Trp Ala Ala Cys Arg
                245                 250                 255
Phe Asp Ser Gln Glu Val Thr Val Arg Val Ala Ser Ser Phe Ile Ser
            260                 265                 270
Val Glu Gln Ala Glu Arg Asn Leu Ala Glu Val Lys Gly Gln Ser Phe
        275                 280                 285
Asp Arg Ile Arg Leu Ala Gly Arg Glu Ala Trp Asn Lys Val Leu Gly
```

```
    290                 295                 300
Arg Ile His Val Glu Gly Gly Thr Lys Asp Glu Arg Thr Thr Phe Tyr
305                 310                 315                 320
Ser Ala Leu Tyr Arg Cys Leu Leu Phe Pro Arg Arg Phe Tyr Glu Glu
                325                 330                 335
Asp Ala Ser Gly Asn Phe Val His Tyr Ser Pro Tyr Asn Gly Glu Val
            340                 345                 350
Leu Pro Gly Tyr Leu Tyr Thr Asp Thr Gly Phe Trp Asp Thr Phe Arg
        355                 360                 365
Ala Leu Phe Pro Leu Leu Asn Leu Leu Tyr Pro Asp Glu Asn Ile Lys
    370                 375                 380
Ile Gln Glu Gly Leu Leu Asn Val Tyr Arg Glu Ser Gly Phe Phe Pro
385                 390                 395                 400
Glu Trp Ala Ser Pro Gly His Arg Asp Cys Met Ile Gly Asn Asn Ser
                405                 410                 415
Ala Ser Val Leu Ala Asp Ala Tyr Leu Lys Gly Val Arg Val Glu Asp
            420                 425                 430
Thr Arg Thr Leu Met Asn Gly Leu Leu His Ala Thr Lys Ala Val His
        435                 440                 445
Pro Lys Ile Ser Ser Thr Gly Arg Lys Gly Trp Glu Trp Tyr Asn Ser
    450                 455                 460
Leu Gly Tyr Val Pro Ala Asp Ala Gly Ile Asp Glu Ser Ala Ala Arg
465                 470                 475                 480
Thr Leu Glu Tyr Ala Tyr Asn Asp Trp Cys Ile Leu Arg Leu Gly Arg
                485                 490                 495
Thr Leu Gly Trp Asp Arg Ala Ala Leu Asp Thr Leu Ala His Arg Ser
            500                 505                 510
Met Asn Tyr Arg His Leu Phe Asp Pro Glu Thr Lys Leu Met Arg Gly
        515                 520                 525
Arg Asn Gln Asp Gly Ser Phe Arg Thr Pro Phe Ser Pro Phe Lys Trp
    530                 535                 540
Gly Asp Val Phe Thr Glu Gly Asn Ala Trp His Tyr Thr Trp Ser Val
545                 550                 555                 560
Phe His Asp Val Gln Gly Leu Ile Asp Leu Met Gly Gly Asp Arg Pro
                565                 570                 575
Phe Val Ser Met Leu Asp Ser Val Phe Asn Thr Pro Pro Met Phe Asp
```

```
            580                 585                 590
Glu Ser Tyr Tyr Gly Phe Val Ile His Glu Ile Arg Glu Met Gln Ile
        595                 600                 605
Ala Asp Met Gly Asn Tyr Ala His Gly Asn Gln Pro Ile Gln His Met
    610                 615                 620
Ile Tyr Leu Tyr Asn His Ala Gly His Pro Trp Lys Ala Gln Glu Arg
625                 630                 635                 640
Leu Arg Glu Val Met Gly Arg Leu Tyr Arg Pro Thr Pro Asp Gly Tyr
                645                 650                 655
Cys Gly Asp Glu Asp Asn Gly Gln Thr Ser Ala Trp Tyr Val Phe Ser
            660                 665                 670
Ala Leu Gly Phe Tyr Pro Val Thr Pro Ala Thr Asp Gln Tyr Val Leu
        675                 680                 685
Gly Ser Pro Ile Phe Ser Lys Val Ile Leu Ser Phe Pro Asp Gly His
    690                 695                 700
Lys Thr Val Leu His Ala Pro Ala Asn Ser Ala Asp Thr Pro Tyr Ile
705                 710                 715                 720
Arg Ser Ile Ser Val Glu Gly Lys Glu Trp Ser Cys Asn Tyr Leu Thr
                725                 730                 735
His Glu Gln Leu Arg Ser Ser Ala Ser Ile Gln Trp Met Met Asp Thr
            740                 745                 750
Lys Pro Asn Tyr Asn Arg Gly Met Lys Glu Ser Asp Arg Pro Tyr Ser
        755                 760                 765
Phe Ser Thr Glu Gln Gln Arg Arg Ala Asn His Ser Asn
    770                 775                 780
```

(2) INFORMATION FOR SEQ ID NO:112

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 446 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112

```
Met Lys Thr Thr Val Gln Gln Ile Ile Leu Cys Leu Ala Leu Met Met
1               5                   10                  15
Ser Gly Val Leu Gly Gly Asn Ala Gln Ser Phe Trp Glu Glu Ile Ala
                20                  25                  30
Pro Pro Phe Ile Ser Asn Glu Pro Asn Val Lys Tyr Ile Ile Pro Asn
        35                  40                  45
Met Gly Ile Asp Ser Lys Gly Thr Ile Tyr Val Thr Val Thr Lys Arg
    50                  55                  60
Ile Gln Gln Gly Ala Asn Tyr Thr Ser Glu Gln Leu Gly Met Tyr Tyr
65                  70                  75                  80
Arg Pro Leu Gly Asp Asn Glu Gln Trp Trp Lys His Asp Pro Tyr Phe
                85                  90                  95
Asp Asp Lys Ile Val Ala Asp Ile Gln Thr Asp Ala Tyr Gly Arg Val
            100                 105                 110
Tyr Val Cys Thr Thr Ser Ser Arg Asp Gln Glu Tyr Gln Leu Tyr Ile
        115                 120                 125
Asn Glu Gln Asn Glu Trp Arg Cys Ile Phe Lys Thr Ser Val Ser Thr
    130                 135                 140
Tyr Glu His Gly Met Ala Val Phe Arg Ser Ser Thr Gly Val Thr Tyr
145                 150                 155                 160
Ile Gly Thr Arg His His Ile Phe Ala Ser Gly Val Asn Asp Phe Glu
                165                 170                 175
Phe Asn Thr Ile Tyr Glu Asp Ser Thr Pro Met Ser Cys Arg Phe Ala
            180                 185                 190
Glu Ala Thr Asn Ser Gly Thr Ile Tyr Leu Ala Leu Met His Glu Thr
        195                 200                 205
```

```
Thr Met Ser Thr Thr Ile Leu Thr Tyr Gln Asn Gly Glu Phe Val Asp
    210                 215                 220
Ile Ser Glu Ser Glu Leu Ser Asn Ser Ile Ile Ala Ser Met Cys Ser
225                 230                 235                 240
Asn Lys Glu Gly Asp Ile Ile Ala Leu Val Thr Ser Tyr Thr Gly Phe
                245                 250                 255
Met Ser Gly Thr Leu Ala Ile Arg Lys Ala Asp Glu Gly Lys Trp Gln
            260                 265                 270
Leu Val Gly Gly Asp Ile Gln Asn Ala Ile Val Gln Asn Ile Cys Met
        275                 280                 285
Met Asp Asp Asn Lys Ile Ala Cys Glu Val Phe Gly Thr Pro Asn Gly
    290                 295                 300
Val Asp Gly Arg Thr Arg Val Cys Val Ser Asp Ala Ser Val Phe Asp
305                 310                 315                 320
Phe Glu Trp Tyr Glu Asp Glu Ile Tyr Gly Gly Leu Ile Phe Asp Thr
                325                 330                 335
Phe Phe Tyr Ser Pro Trp Asp Lys Leu Leu Tyr Ala Lys Phe Gly Gly
            340                 345                 350
Ile Met Leu Arg Ser Lys Glu Ser Phe Ile Thr Ser Phe Ile Ser Pro
        355                 360                 365
Thr Val Val Gln Gly Val Asp Val Tyr Thr Leu Ala Gly Lys Ile Arg
    370                 375                 380
Ile Glu Ser Glu Thr Pro Val Ser Glu Val Leu Leu Phe Asp Leu Ala
385                 390                 395                 400
Gly Arg Met Val Leu Arg Gln Thr Ile Asp Asn Lys Ile Tyr Ser Asp
                405                 410                 415
Ile Asp Thr Asn Gly Leu Lys Arg Ser Gly Ile Tyr Val Val Ser Val
            420                 425                 430
Arg Leu Ser Ser Gly Gln Val Phe Ser His Lys Val Gln Val
        435                 440                 445
```

(2) INFORMATION FOR SEQ ID NO:113

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

```
Met Ile Ile Arg Cys Leu Ile Arg Arg Pro Arg Thr Val Leu Phe Gly
1               5                   10                  15
Leu Ile Phe Val Val Gly Leu Phe Ser Ala Met Ala Gln Glu Lys Lys
            20                  25                  30
Asp Ser Leu Ser Thr Val Gln Pro Val Pro Asn Ser Ser Met Val Glu
        35                  40                  45
Gln Thr Pro Leu Leu Ser Ile Asp His Pro Val Leu Pro Ala Ser Phe
    50                  55                  60
Gln Asn Thr Arg Thr Leu Lys Arg Phe Arg Asp Lys His Leu Ser Asp
65                  70                  75                  80
Ala Leu Leu Asn Gly Leu Lys Pro His Arg Ser Ser Leu Gln Leu Asn
                85                  90                  95
Glu Glu Leu Asn Phe Ala Ala Glu Arg Arg Asp Phe Val Ser Pro Leu
            100                 105                 110
Leu Gln Thr Arg His Ala Ala Gly Val Leu Ser Trp Arg Pro Thr Asp
        115                 120                 125
Arg Met His Phe Tyr Thr Ser Gly Asn Ile Gly Leu Gly His Asp Leu
    130                 135                 140
Leu Thr Gly Val Arg Lys Asp Phe Gly Trp Asn Ala Gly Ala Asp Phe
145                 150                 155                 160
Leu Leu Ser Gln Asn Leu Thr Ala His Val Gln Gly Gly Trp Gln Gln
```

```
                165                 170                 175
Asn Phe Gly Phe Ile Pro Met Thr Ala Val Asn Gly Gln Leu Arg Trp
            180                 185                 190
Gln Ala Thr Glu Arg Leu Ser Phe Thr Thr Gly Ile Asp Tyr Arg Gln
        195                 200                 205
Val Gln Trp Asn Ala Phe Asp Asn Arg Thr Phe Ser Leu Lys Gly Ser
    210                 215                 220
Ala Arg Tyr Glu Val Met Asp Asn Val Phe Val Asn Gly Phe Gly Ser
225                 230                 235                 240
Tyr Pro Leu Tyr Ser Ser Thr Arg Ser Gly Leu Asn Met Ala Val Pro
                245                 250                 255
Met His Gly Phe Gly Pro Gln Tyr Gly Gly Ser Leu Glu Leu Lys Val
            260                 265                 270
Ser Glu Arg Phe Gly Phe Ala Val Gly Met Glu Arg Glu Tyr Asn Ile
        275                 280                 285
Trp Thr Arg Arg Trp Glu Thr His Tyr Phe Ala Tyr Pro Val Phe Tyr
    290                 295                 300
Gly Asp Lys Lys
305
```

(2) INFORMATION FOR SEQ ID NO:114

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114

```
Met Lys Arg Ile Phe Thr Val Ala Leu Val Leu Leu Ala Ser Val Thr
1               5                   10                  15
Met Ala Ile Gly Gln Ser Arg Pro Ala Leu Arg Val Asp Ala Asn Phe
            20                  25                  30
Val Gly Ser Asn Gln Ser Met Lys Arg Asp Gly Tyr Val Trp Asp Thr
        35                  40                  45
Lys Met Asn Val Gly Leu Arg Val Gly Ala Ala Ala Glu Phe Met Ile
    50                  55                  60
Gly Ser Arg Gly Phe Tyr Leu Ala Pro Gly Leu Asn Tyr Thr Met Lys
65                  70                  75                  80
Gly Ser Lys Thr Glu Trp Asp Ile Pro Glu Met Val Pro Gly Thr Tyr
                85                  90                  95
Ile Thr Met Val Ser Thr Arg Leu His Tyr Leu Gln Leu Pro Ile Asn
            100                 105                 110
Ala Gly Met Arg Phe Asp Leu Met Asn Asp Met Ala Val Ser Ile Glu
        115                 120                 125
Ala Gly Pro Phe Leu Ala Tyr Gly Ile Tyr Gly Thr Tyr Arg Gln Lys
    130                 135                 140
Leu Glu Gly Trp Lys Pro Asn Asn Tyr Ser Thr Glu Phe Phe Gly Pro
145                 150                 155                 160
Thr Leu Gly Gly Pro Thr Asn Ile Arg Trp Asp Ile Gly Ala Asn Ile
                165                 170                 175
Ile Ala Ala Phe His Tyr Lys Arg Tyr Tyr Ile Gln Ile Gly Tyr Glu
            180                 185                 190
His Gly Phe Val Asp Ile Val Ser Gly Gly Gly Ser Asp Ile Pro Arg
        195                 200                 205
Leu Asn Asp Asn Arg Gln Ser Ser Ser Thr Thr Ala Leu Arg Glu Lys
    210                 215                 220
Gly Asn Asn Glu Tyr Ala Tyr Asn Arg Asp Phe Phe Val Gly Ile Gly
225                 230                 235                 240
Tyr Arg Phe
```

(2) INFORMATION FOR SEQ ID NO:115

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115

```
Met Lys Thr Lys Val Leu Arg Lys Phe Val Val Ala Ala Phe Ala Val
1               5                   10                  15
Ala Thr Leu Cys Pro Leu Ala Gln Ala Gln Thr Met Gly Gly Asp Asp
            20                  25                  30
Val Lys Val Val Gln Tyr Asn Gln Glu Lys Leu Val Gln Thr Arg Met
        35                  40                  45
Ser Val Ala Asp Asn Gly Trp Ile Tyr Val Met Thr His Ser Gly Tyr
    50                  55                  60
Asp Thr Gly Asn Ser Asn Val Lys Ile Phe Arg Ser Lys Asp Gln Gly
65                  70                  75                  80
Ala Thr Tyr Gln Lys Leu Arg Asp Trp Asp Pro Ser Asp Asp Tyr Gln
                85                  90                  95
Phe Gln Asp Phe Asp Ile Val Val Thr Gly Lys Asn Glu Ser Asp Ile
            100                 105                 110
Lys Ile Trp Ser Val Glu Leu Met Asn Lys Pro Gly Gly Tyr Lys Ser
```

115 120 125
Arg Val Ala Val Phe Ser Arg Asp Ala Asn Ala Gln Asn Ala Lys Leu
130 135 140
Val Tyr Lys Glu Asp Phe Ser Asn Val Gln Leu Tyr Asp Val Asp Ile
145 150 155 160
Ala Ser Asn Tyr Arg Ser Pro Ser Ser Leu Asn Asn Gly Gly Asn Pro
165 170 175
Phe Ala Leu Ala Phe Ala Tyr Thr Gly Phe Asn Asn Thr His Lys Ile
180 185 190
Ser Phe Val Asp Tyr Val Phe Ser Leu Asn Gly Gly Gln Asn Phe Asn
195 200 205
Lys Asn Leu Leu Phe Ser Gln Asp Gly Glu Lys Lys Ile Asp Lys Val
210 215 220
Asp Leu Ser Leu Gly Ser Thr Ser Glu Ser Met Gly His Asn Ala Trp
225 230 235 240
Pro Leu Met Gly Val Val Phe Glu Met Asn Lys Gln Gly Gly Lys Ser
245 250 255
Asp Ile Gly Phe Leu Ser Asn Phe Val Asp Asn Asp Pro Glu Phe Gln
260 265 270
Trp Ser Gly Pro Ile Lys Val Ser Glu Ser Asp Met Ser Phe Ser Pro
275 280 285
Lys Ile Gln Met Leu Leu Asp Glu Asp Asn Asn Thr Ile Asn Gly Glu
290 295 300
Ser Cys His Asn Phe Met Ile Thr Tyr Ser Asp Tyr Asp Ser Glu Tyr
305 310 315 320
Ser Asp Trp Asp Ile Arg Tyr Val Tyr Pro Lys Lys Ser Phe Lys Tyr
325 330 335
Glu Lys Gly Lys Thr Pro Thr Met Asp Asp Leu Val Glu Ala Phe Leu
340 345 350
Thr Ala Ser Tyr Gln Ser Glu Thr Asn Ser Gly Leu Gly Tyr Asp Lys
355 360 365
Asn Ala Asn His Tyr Leu Ile Thr Tyr Ala Lys Lys Glu Glu Asn Gly
370 375 380
Thr Asn Thr Leu Lys Tyr Arg Trp Ala Asn Tyr Asp Lys Ile His Asn
385 390 395 400
Lys Asp Leu Trp Ser Asp Thr Phe Thr Tyr Thr Ser Ser Ala Asn Ala

```
                    405                     410                     415
Leu Tyr Thr Pro Gln Val Asp Ile Asn Pro Thr Lys Gly Leu Val Cys
                420                     425                     430
Trp Ser Trp Val Glu Tyr Leu Pro Gly Lys Arg Ile Val Trp Ser Asp
            435                     440                     445
Thr Gln Trp Thr His Ala Asn Gly Val Glu Asp Ile Val Met Gln Glu
    450                     455                     460
Gly Ser Met Lys Leu Tyr Pro Asn Pro Ala Gln Glu Tyr Ala Val Ile
465                 470                     475                     480
Ser Leu Pro Thr Ala Ala Asn Cys Lys Ala Val Val Tyr Asp Met Gln
                    485                     490                     495
Gly Arg Val Val Ala Glu Ala Ser Phe Ser Gly Asn Glu Tyr Arg Leu
                500                     505                     510
Asn Val Gln His Leu Ala Lys Gly Thr Tyr Ile Leu Lys Val Val Ser
            515                     520                     525
Asp Thr Glu Arg Phe Val Glu Lys Leu Ile Val Glu
    530                     535                     540
```

(2) INFORMATION FOR SEQ ID NO:116

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
- (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116

```
Met Lys Lys Thr Thr Leu Thr Gly Ser Ile Cys Ala Leu Leu Leu Phe
1               5                   10                  15
Leu Gly Leu Ser Ala Asn Ala Gln Ser Lys Leu Lys Ile Lys Ser Ile
            20                  25                  30
Glu Ala Ala Thr Thr Phe Ser Ser Ala Thr Ala Gly Asn Gly Phe Gly
        35                  40                  45
Gly Asn Ile Phe Gly Met Asp Met Ser Ile Arg Met Arg Val His His
    50                  55                  60
Ser Ile Leu Pro Glu Gly Leu Asp Phe Ser Val Gly Ile His Glu Arg
65                  70                  75                  80
Arg Ala His Trp Glu Glu Ala Gly Ser Pro Lys Leu Met Tyr Thr Asn
                85                  90                  95
Val Pro Ser Ile Ile Gly Ile Val Glu Lys Val Ile Val Phe Glu Asp
            100                 105                 110
Ala Glu Asp Phe Phe Asp Lys Lys Ala Leu Gly Arg Phe Leu Ile Ser
        115                 120                 125
Leu Gly Ile Ser Tyr Thr Lys His Leu Gly Ala Tyr Trp Gly Trp Thr
    130                 135                 140
Asn Asp Ala His Ile Leu Phe Ser Pro Ile Pro Lys Ser Lys Val His
145                 150                 155                 160
Tyr Asp Thr Tyr Thr Arg Ala Gly Ser Asp Leu Val Leu Gln Ser Glu
                165                 170                 175
Asp Val Ala Thr Val Ser Asn Gly Phe Ser Pro Gly Ile Gly Leu Lys
            180                 185                 190
Ser Ser Ile Trp Trp Lys Met Pro Ile Lys Ser Lys Tyr Asp Phe Arg
        195                 200                 205
Leu Gly Phe Ser Leu Gly Tyr Glu Tyr Leu Asn Leu Leu Tyr Pro Tyr
    210                 215                 220
Arg Asn Phe Lys Leu Asp Gly Asn Lys Pro Leu Ser Ala Leu Ser Pro
225                 230                 235                 240
Arg Met Asn His Ile Gly His Val Gly Phe Asn Phe Thr Val Gly Leu
                245                 250                 255
Trp Thr Asn
```

(2) INFORMATION FOR SEQ ID NO:117

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117

```
Met Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser
1               5                   10                  15
Leu Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys
            20                  25                  30
Ser Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg
        35                  40                  45
Ala Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr
    50                  55                  60
Pro Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe
65                  70                  75                  80
Gly Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly
                85                  90                  95
Tyr Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala
            100                 105                 110
Asn Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln
```

```
        115                 120                 125
Glu Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile
    130                 135                 140
Asn Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg
145                 150                 155                 160
Phe Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp
                165                 170                 175
Ile Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly
            180                 185                 190
Gln Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala
        195                 200                 205
Ile Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met
    210                 215                 220
Ile Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala
225                 230                 235                 240
Ala Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu
                245                 250                 255
Ala Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:118

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 270 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
 (A) NAME/KEY: misc_feature

(B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118

```
Met Lys Ser Met Arg Ser Val Leu Leu Leu Leu Phe Pro Leu Ser Leu
1               5                   10                  15
Ile Thr Ala Leu Gly Cys Ser Asn Asn Lys Ala Ala Glu Ser Lys Ser
            20                  25                  30
Val Ser Phe Asp Ser Ala Tyr Leu Glu Arg Tyr Ile Pro Leu Arg Ala
        35                  40                  45
Asp Ile Asp Thr Pro Ser Leu His Val Met Ile Ser Tyr Val Tyr Pro
    50                  55                  60
Ser Gly Asp Asp Met Leu Thr Glu Ile Phe Asn Gly Leu Leu Phe Gly
65                  70                  75                  80
Asp Ser Leu Met Asp Ser Ser Ser Pro Glu Asn Ala Met Glu Gly Tyr
                85                  90                  95
Ala Gln Met Leu Gly Glu Asp Tyr Arg Ser Asn Asn Ala Glu Ala Asn
            100                 105                 110
Leu Gln Gly Leu Pro Ser Asp Leu Leu Asp Tyr Ile Tyr Lys Gln Glu
        115                 120                 125
Asn Thr Ile Ala Tyr Cys Asp Thr Gly Leu Ile Ser Thr Arg Ile Asn
    130                 135                 140
Thr Tyr Thr Tyr Glu Gly Gly Ala His Thr Glu Asn Thr Val Arg Phe
145                 150                 155                 160
Ala Asn Ile Leu Arg Thr Thr Gly Lys Val Leu Glu Glu Arg Asp Ile
                165                 170                 175
Phe Lys Ile Asp Tyr Ala Glu Arg Leu Ser Ala Leu Ile Ile Gly Gln
            180                 185                 190
Leu Val His Asp Phe Gly Lys Thr Thr Pro Ala Glu Leu Asp Ala Ile
        195                 200                 205
Gly Phe Phe Asn Ala Glu Glu Ile Gln Pro Asn Gly Asn Phe Met Ile
    210                 215                 220
Asp Asp Lys Gly Leu Thr Tyr Cys Phe Asn Glu Tyr Gln Ile Ala Ala
225                 230                 235                 240
Tyr Ala Arg Gly Ala Val Tyr Val Arg Leu Gly Tyr Asp Val Leu Ala
                245                 250                 255
```

```
Pro Leu Leu Arg Asp Asp Ser Pro Leu Lys Arg Tyr Leu Pro
            260                 265                 270
```

(2) INFORMATION FOR SEQ ID NO:119

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119

```
Met Val Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val
1               5                   10                  15
Leu Leu Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu
            20                  25                  30
Asp Asp Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val
        35                  40                  45
Lys Asp Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr
    50                  55                  60
Thr Val Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly
65                  70                  75                  80
Gln Ser Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser
                85                  90                  95
Thr Arg Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe
```

```
            100                 105                 110
Tyr Lys Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val
        115                 120                 125
Thr Asp Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp
    130                 135                 140
Ala Ser Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe
145                 150                 155                 160
Pro Tyr Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr
                165                 170                 175
Trp Asn Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly
            180                 185                 190
Tyr Tyr Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe
        195                 200                 205
Tyr Asn Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp
    210                 215                 220
Gly Ser Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr
225                 230                 235                 240
His His Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala
                245                 250                 255
Tyr Tyr Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly
            260                 265                 270
Ala Lys Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser
        275                 280                 285
Gln Lys Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu
    290                 295                 300
Gln Asn Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn
305                 310                 315                 320
Ile Glu Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val
                325                 330                 335
Phe Gln Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile
            340                 345                 350
Arg Ser Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro
        355                 360                 365
Ser Arg Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser
    370                 375                 380
Ser Gly Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
```

```
385                 390                 395                 400
```

(2) INFORMATION FOR SEQ ID NO:120

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 398 amino acids
  (B) TYPE: amino acid
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
  (A) NAME/KEY: misc_feature
  (B) LOCATION 1...398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120

```
Met Lys Leu Ile Lys Arg Ser Leu Leu Leu Leu Gly Ala Val Leu Leu
1               5                   10                  15
Ile Thr Leu Pro Ala Tyr Ser Gln Asn Asp Asp Ile Phe Glu Asp Asp
            20                  25                  30
Ile Tyr Thr Ser Arg Lys Glu Ile Arg Lys Gln Asn Gln Val Lys Asp
        35                  40                  45
Trp Gln Asn Gln Glu Asp Gly Tyr Gly Asp Asp Thr Glu Tyr Thr Val
    50                  55                  60
Ala Ser Asp Arg Asp Ile Asp Ala Tyr Asn Arg Arg Asp Gly Gln Ser
65                  70                  75                  80
Tyr Asp Gly Lys Lys Leu Ser Lys Asp Lys Lys Arg Asp Ser Thr Arg
                85                  90                  95
Ser Ser Val Pro Gly Arg Tyr Ser Arg Arg Leu Ala Arg Phe Tyr Lys
            100                 105                 110
```

```
Pro Asn Thr Ile Val Ile Ser Gly Ala Asp Asn Val Tyr Val Thr Asp
        115                 120                 125
Asp Gly Glu Tyr Phe Val Tyr Gly Asp Glu Tyr Tyr Asp Asp Ala Ser
    130                 135                 140
Ser Val Asn Ile Tyr Ile Asn Ser Pro Trp Cys Asp Pro Phe Pro Tyr
145                 150                 155                 160
Thr Ser Trp Tyr Pro Ser Phe Ser Gly Trp Tyr Asn Tyr Thr Trp Asn
                165                 170                 175
Tyr Pro Trp Phe Tyr Tyr Gly Ser His Ile Gly Trp Gly Gly Tyr Tyr
            180                 185                 190
Pro Gly Tyr Asn Trp Tyr Trp Ser Tyr Tyr Tyr Asp Pro Phe Tyr Asn
        195                 200                 205
Pro Tyr Gly Ile Gly Met Gly Trp Gly Tyr Pro Tyr Gly Trp Gly Ser
    210                 215                 220
Tyr Tyr Gly Trp Gly Gly Tyr Pro Gly Val Ile His His Tyr His His
225                 230                 235                 240
Tyr Pro Lys Lys Thr Tyr Ser Asn Gly Gln His Ser Gly Ala Tyr Tyr
                245                 250                 255
Ser Tyr Gly Arg Pro Asn Arg Ile Lys Gly Gly Thr Ser Gly Ala Lys
            260                 265                 270
Leu Gly Thr Gly Arg Tyr Asp Arg Ile Gln Asn Ser Ser Ser Gln Lys
        275                 280                 285
Asn Lys Phe Gly Leu Gln Ser Asn Lys Pro Asn Asn Asn Leu Gln Asn
    290                 295                 300
Val Lys Ser Gly Arg Thr Gly Arg Ala Asn Arg Asp Arg Asn Ile Glu
305                 310                 315                 320
Thr Val Thr Pro Asn Asn Gly Gln Lys Gln Asn Arg Pro Val Phe Gln
                325                 330                 335
Gln Asn Gln Ser Gly Asn Asp Arg Pro Thr Gly Arg Asn Ile Arg Ser
            340                 345                 350
Glu Arg Gln Gly Glu Asn Asn Asp Arg Thr Phe Ser Thr Pro Ser Arg
        355                 360                 365
Ser Asn Ser Asn Gly Gly Phe Ser Thr Pro Ser Arg Ser Ser Ser Gly
    370                 375                 380
Ser Met Ser Gly Gly Gly Gly Arg Ser Gly Arg Gly Arg Asn
385                 390                 395
```

(2) INFORMATION FOR SEQ ID NO:121

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121

```
Met Lys Arg Met Leu Leu Leu Leu Val Val Leu Leu Tyr Gly Ile Ala
1               5                   10                  15
Gly Arg Leu Ala Ala Gln Asp Val Ile Arg Pro Trp Ser Leu Gln Val
            20                  25                  30
Gly Ala Gly Tyr Ser Asp Thr Glu Asn Ile Pro Gly Gly Phe Thr Tyr
        35                  40                  45
Gly Phe Tyr Leu Gly Lys Arg Met Gly Ser Phe Leu Glu Val Gly Leu
    50                  55                  60
Ser Met Tyr Asn Ser Thr Arg Gln Thr Ala Asn Asn Ala Asp Ser Phe
65                  70                  75                  80
Ala Ser Asn Glu Gly Asp Gly Ser Phe Gln Val Asn Met Ser Ser Pro
                85                  90                  95
Asn Glu Lys Trp Ser Phe Phe Asp Ala Gly Ser Ala Asn Cys Tyr Met
            100                 105                 110
Ile Val Val Gly Val Asn Pro Leu His Leu Phe Trp Gln Asn Ser Arg
```

115 120 125

His Asn Leu Phe Leu Ala Val Gln Ala Gly Leu Ser Asn Lys His Asn

130 135 140

Ile His Phe Ile Tyr Gly Asp Lys Gly Ala Lys Val Ser Ile Tyr Thr

145 150 155 160

Asn Ser Asn Thr Tyr Ile Gly Tyr Gly Ala Arg Val Ala Tyr Glu Tyr

165 170 175

Gln Ile His Lys Asn Val Gly Ala Gly Ala Ala Val Met Tyr Asp His

180 185 190

Gly Asn Lys Met Leu Thr Ala Met Ala Thr Leu Ser Thr His Phe

195 200 205

(2) INFORMATION FOR SEQ ID NO:122

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 771 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122

Met Leu Thr Ile Arg Asn Phe Leu Leu Phe Cys Cys Leu Ser Leu Ile

1 5 10 15

Ala Phe Ala Ala Asp Ala Gln Ser Ser Val Ser Ser Gly Arg Arg Leu

20 25 30

```
Thr Glu Tyr Val Asn Pro Phe Ile Gly Thr Ala Asn Tyr Gly Thr Thr
        35                  40                  45
Asn Pro Gly Ala Val Leu Pro Asn Gly Leu Met Ser Val Thr Pro Phe
    50                  55                  60
Asn Val Ser Gly Ser Thr Glu Asn Arg Phe Asp Lys Asp Ser Arg Trp
65                  70                  75                  80
Trp Ser Ala Pro Tyr Ser Ala Asp Asn Ser Tyr Cys Ile Gly Phe Ser
                85                  90                  95
His Val Asn Leu Ser Gly Val Gly Cys Pro Glu Leu Ser Gly Ile Leu
            100                 105                 110
Leu Met Ala Thr Ser Gly Thr Phe Asp Pro Asp Tyr Cys Cys Tyr Gly
        115                 120                 125
Ser Ser Leu Ser Arg Glu Tyr Ala Arg Pro Gly Glu Tyr Lys Ala Val
    130                 135                 140
Leu Asp Lys Tyr Gly Ile Asp Ala Ala Val Thr Val Thr Glu Arg Thr
145                 150                 155                 160
Ala Leu Thr Glu Phe Ala Phe Pro Glu Gly Glu Gly His Ile Leu Leu
                165                 170                 175
Asn Leu Gly Gln Ala Leu Ser Asn Glu Ser Gly Ala Ser Val Arg Phe
            180                 185                 190
Leu Asn Asp Ser Thr Val Val Gly Ser Arg Leu Met Gly Thr Phe Cys
        195                 200                 205
Tyr Asn Pro Gln Ala Val Phe Arg Gln Tyr Phe Val Leu Gln Val Ser
    210                 215                 220
Arg Arg Pro Ile Ser Ala Gly Tyr Trp Lys Lys Gln Pro Pro Met Thr
225                 230                 235                 240
Val Glu Ala Gln Trp Asp Ser Thr Ala Gly Lys Tyr Lys Gln Tyr Asp
                245                 250                 255
Gly Tyr Lys Arg Glu Met Ser Gly Asp Asp Ile Gly Val Arg Phe Ser
            260                 265                 270
Phe Asn Cys Asp Gln Gly Glu Lys Ile Tyr Val Arg Ser Ala Val Ser
        275                 280                 285
Phe Val Ser Glu Ala Asn Ala Leu Tyr Asn Leu Glu Ala Glu Gln Glu
    290                 295                 300
Glu Val Phe Lys Ser Val Gly Gly Asn Pro Ala Lys Ala Phe Ser Ala
305                 310                 315                 320
```

```
Ile Arg Ser Arg Ala Ile Glu Arg Trp Glu Glu Ala Leu Gly Thr Val
                325                 330                 335
Glu Val Glu Gly Gly Thr Pro Asp Glu Lys Thr Ile Phe Tyr Thr Ala
            340                 345                 350
Leu Tyr His Leu Leu Ile His Pro Asn Ile Leu Gln Asp Ala Asn Gly
        355                 360                 365
Glu Tyr Pro Met Met Gly Ser Gly Lys Thr Gly Asn Thr Ala His Asp
    370                 375                 380
Arg Tyr Thr Val Phe Ser Leu Trp Asp Thr Tyr Arg Asn Val His Pro
385                 390                 395                 400
Leu Leu Cys Leu Leu Tyr Pro Glu Lys Gln Leu Asp Met Val Arg Thr
                405                 410                 415
Leu Ile Asp Met Tyr Arg Glu Ser Gly Trp Leu Pro Arg Trp Glu Leu
            420                 425                 430
Tyr Gly Gln Glu Thr Leu Thr Met Glu Gly Asp Pro Ser Leu Ile Val
        435                 440                 445
Ile Asn Asp Thr Trp Gln Arg Gly Leu Arg Ala Phe Asp Thr Ala Thr
    450                 455                 460
Ala Tyr Glu Ala Met Lys Lys Asn Ala Ser Ser Ala Gly Ala Thr His
465                 470                 475                 480
Pro Ile Arg Pro Asp Asn Asp Asp Tyr Leu Thr Leu Gly Phe Val Pro
                485                 490                 495
Leu Arg Glu Gln Tyr Asp Asn Ser Val Ser His Ala Leu Glu Tyr Tyr
            500                 505                 510
Leu Ala Asp Trp Asn Leu Ser Arg Phe Ala His Ala Leu Gly His Lys
        515                 520                 525
Glu Asp Ala Ala Leu Phe Gly Lys Arg Ser Leu Gly Tyr Arg His Tyr
    530                 535                 540
Tyr Asn Lys Glu Tyr Gly Met Leu Cys Pro Leu Leu Pro Asp Gly Ser
545                 550                 555                 560
Phe Leu Thr Pro Phe Asp Pro Lys Gln Gly Glu Asn Phe Glu Pro Asn
                565                 570                 575
Pro Gly Phe His Glu Gly Ser Ala Tyr Asn Tyr Ala Phe Phe Val Pro
            580                 585                 590
His Asp Ile Gln Gly Leu Ala Arg Leu Met Gly Gly Ala Lys Val Phe
        595                 600                 605
```

```
Ser Glu Arg Leu Gln Lys Val Phe Asp Glu Gly Tyr Tyr Asp Pro Thr
    610                 615                 620
Asn Glu Pro Asp Ile Ala Tyr Pro Tyr Leu Phe Ser Tyr Phe Pro Lys
625                 630                 635                 640
Glu Ala Trp Arg Thr Gln Lys Leu Thr Arg Glu Leu Ile Asp Lys His
                645                 650                 655
Phe Cys Asn Ala Pro Asn Gly Leu Pro Gly Asn Asp Asp Ala Gly Thr
            660                 665                 670
Met Ser Ala Trp Leu Val Tyr Ser Met Leu Gly Phe Tyr Pro Asp Cys
        675                 680                 685
Pro Gly Ser Pro Thr Tyr Thr Leu Thr Ser Pro Val Phe Pro Arg Val
    690                 695                 700
Arg Ile Arg Leu Asn Pro Gln Tyr Tyr Pro Gln Gly Glu Leu Ile Ile
705                 710                 715                 720
Thr Thr Asn Thr Glu Asn Gln Pro Thr Asp Ser Ile Tyr Ile His Thr
                725                 730                 735
Val Ser Leu Gly Asn Lys Thr Leu Pro His Gly Thr Arg His Ile Ser
            740                 745                 750
His Ala Asp Leu Val Arg Cys Gly His Leu Arg Tyr Glu Leu Ser Asn
        755                 760                 765
Arg Pro Arg
    770
```

(2) INFORMATION FOR SEQ ID NO:123

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 951 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123

```
Met Arg Val Ser Asp Leu Cys Ser Arg Leu Ser Trp Leu Leu Pro Val
1               5                   10                  15
Ile Leu Val Gly Leu Leu Cys Ala Thr Leu Val Ala Ala Glu Arg Pro
            20                  25                  30
Met Ala Gly Ala Val Gly Leu His His Arg Arg His Ala Ala Leu Ser
        35                  40                  45
Asp Ser Thr Ala Lys Asp Thr Val Pro Leu Ala Lys Pro Ile Pro Asp
    50                  55                  60
Ser Ala Phe Arg Asp Ser Leu Pro Ala Asp Ser Thr Gly Ser Met Arg
65                  70                  75                  80
Gln Asp Ser Val Tyr Asp Asp Glu Phe Glu Leu Glu Asp Ile Val Glu
                85                  90                  95
Tyr Glu Ala Ala Asp Ser Ile Val Leu Leu Gly Gln Asn Arg Ala Tyr
            100                 105                 110
Leu Phe Gly Lys Ser Tyr Val Ser Tyr Gln Lys Ser Arg Leu Glu Ala
        115                 120                 125
Asn Phe Met Tyr Leu Asn Thr Asp Ser Ser Thr Val Tyr Thr Arg Tyr
    130                 135                 140
Val Leu Asp Thr Ala Gly Tyr Pro Met Ala Phe Pro Val Phe Lys Asp
145                 150                 155                 160
Gly Glu Gln Ser Phe Glu Ala Lys Asn Phe Thr Tyr Asn Phe Arg Thr
                165                 170                 175
Glu Lys Gly Ile Ile Ser Gly Val Ile Thr Gln Gln Gly Glu Gly Tyr
            180                 185                 190
Leu Thr Ala Gly Lys Thr Lys Lys Met Pro Asp Asn Ile Met Phe Met
        195                 200                 205
Gln Gly Gly Arg Tyr Thr Thr Cys Asp Asn His Asp His Pro His Phe
    210                 215                 220
Tyr Ile Asn Leu Ser Lys Ala Lys Val His Pro Glu Lys Asp Ile Val
```

```
225                 230                 235                 240
Thr Gly Pro Val Asn Leu Val Ile Ala Asp Met Pro Leu Pro Ile Gly
                245                 250                 255
Leu Pro Phe Gly Tyr Phe Pro Phe Ser Asn Lys Tyr Ser Ser Gly Ile
            260                 265                 270
Leu Met Pro Thr Tyr Gly Glu Asp Asn Arg Tyr Gly Phe Tyr Leu Arg
        275                 280                 285
Asn Gly Gly Tyr Tyr Phe Ala Phe Ser Asp Tyr Ile Asp Leu Ala Leu
    290                 295                 300
Arg Gly Glu Ile Phe Ser Lys Gly Ser Trp Gly Ile Ser Ala Gln Ser
305                 310                 315                 320
Lys Tyr Lys Lys Arg Tyr Lys Tyr Asn Gly Ser Phe Glu Ala Asn Tyr
                325                 330                 335
Leu Val Ser Lys Ser Gly Asp Lys Tyr Val Pro Gly Asp Tyr Ser Lys
            340                 345                 350
Thr Thr Ser Leu Asn Ile Arg Trp Thr His Ser Gln Asp Pro Lys Ala
        355                 360                 365
Asn Pro Leu Gln Thr Leu Ser Ala Asn Val Asn Phe Ala Thr Gly Ser
    370                 375                 380
Tyr Phe Gln Asn Ser Leu Asn Thr Thr Tyr Asp Val Asn Ala Arg Thr
385                 390                 395                 400
Ala Thr Thr Arg Ser Ser Ala Val Ser Tyr Ser Arg Lys Phe Pro Gly
                405                 410                 415
Thr Pro Phe Ser Ile Thr Gly Ser Met Asp Ile Ser Gln Asn Met Arg
            420                 425                 430
Asp Thr Thr Val Ser Leu Thr Leu Pro Asn Leu Ser Ile Asn Met Ser
        435                 440                 445
Thr Arg Tyr Pro Phe Lys Arg Lys Thr Arg Val Gly Pro Glu Arg Trp
    450                 455                 460
Tyr Glu Lys Leu Ser Val Gly Tyr Ser Gly Gln Leu Arg Asn Ser Ile
465                 470                 475                 480
Leu Thr Lys Glu Lys Asp Leu Leu Gln Ser Asn Leu Val Arg Asp Trp
                485                 490                 495
Lys Asn Gly Met Arg His Ser Val Pro Ile Ser Leu Thr Val Pro Leu
            500                 505                 510
Leu Asp Tyr Ile Asn Leu Thr Met Gly Val Asn Tyr Asn Glu Trp Trp
```

```
        515                 520                 525
Tyr Thr Lys Gly Ile Arg Lys Ser Trp Asn Glu Asp Lys Lys Thr Phe
    530                 535                 540
Leu Pro Ser Asp Thr Thr Tyr Lys Phe Arg Arg Leu Tyr Asp Tyr Ser
545                 550                 555                 560
Leu Ser Ala Gly Leu Ser Thr Thr Leu Tyr Gly Met Phe Lys Pro Trp
                565                 570                 575
Lys Pro Phe Ser Phe Gly Gly Asn Leu Ile Met Ile Arg His Arg Phe
            580                 585                 590
Thr Pro Thr Val Ser Phe Ser Tyr Met Pro Asp Phe Thr Lys Arg Arg
        595                 600                 605
Tyr Gly Phe Trp Glu Leu Leu Glu His Thr Asp Gln Asn Gly Lys Leu
    610                 615                 620
His Thr Leu Leu Tyr Ser Pro Tyr Phe Glu Gln Ile Phe Gly Ala Pro
625                 630                 635                 640
Ser Met Gly Asn Ala Gly Ser Val Asn Phe Ser Phe Asp Asn Asn Leu
                645                 650                 655
Glu Ala Lys Ile Lys Ser Lys Ser Asp Ser Thr Gly Ile Lys Lys Ile
            660                 665                 670
Ser Leu Ile Asp Gln Phe Thr Trp Ser Thr Ser Tyr Asn Met Phe Ala
        675                 680                 685
Asp Ser Ile Arg Trp Ser Asn Ile Ser Ala Ser Leu Ala Leu Arg Leu
    690                 695                 700
Ser Lys Ser Phe Thr Leu Arg Leu Ser Gly Leu Phe Asp Pro Tyr Leu
705                 710                 715                 720
Thr Lys Tyr Tyr Glu Gly Glu Asp Gly Lys Ile Ile Pro Tyr Lys Ser
                725                 730                 735
Asn Asp Leu Arg Ile Phe Asn Gly Lys Gly Leu Ala Arg Leu Ile Ser
            740                 745                 750
Thr Gly Thr Ser Phe Ser Tyr Thr Leu Asn Lys Glu Ser Leu Ser Gly
        755                 760                 765
Leu Ile Ala Leu Phe Ser Gly Lys Lys Glu Arg Arg Asp Glu Lys Lys
    770                 775                 780
Asn Thr Gly Ala Thr Pro His Glu Gly Asp Asp Ala Ala Asp Ile Leu
785                 790                 795                 800
Glu Gly Gly Arg Pro Gln Asn Glu Ser Gly Gly Ser Leu Leu Glu Arg
```

```
                805                 810                 815
Asn Arg Gln Gly Gly Ala Val Asp Gln Asp Gly Tyr Phe Ala Tyr Ser
            820                 825                 830
Ile Pro Trp Ser Leu Ser Phe Asp Tyr Ser Trp Asn Ile Ala Thr Asp
        835                 840                 845
Tyr Asn Arg Tyr Asn Val Asn Lys Met Glu His Tyr Tyr Arg Val Thr
    850                 855                 860
Gln Asn Leu Ser Phe Arg Gly Asn Ile Gln Pro Thr Pro Asn Trp Ser
865                 870                 875                 880
Phe Gly Phe Asn Ala Asn Tyr Asn Phe Asp Leu Lys Lys Ile Thr Ser
                885                 890                 895
Leu Thr Cys Asn Val Thr Arg Asp Met His Cys Trp Ala Ile Ser Ala
            900                 905                 910
Ser Phe Ile Pro Ile Gly Ala Tyr Lys Ser Tyr Asn Phe Val Ile Ser
        915                 920                 925
Val Lys Ser Ser Leu Leu Gln Asp Leu Lys Tyr Gln Gln Ser Asn Arg
    930                 935                 940
Pro Ile Thr Asn Thr Trp Tyr
945                 950
```

(2) INFORMATION FOR SEQ ID NO:124

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 581 amino acids
  (B) TYPE: amino acid
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
  (A) NAME/KEY: misc_feature

(B) LOCATION 1...581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124

```
Met Ile Arg Lys Leu Ile Leu Leu Leu Ala Leu Met Pro Val Ala Ser
1               5                   10                  15
Val Ala Phe Ala Val Pro Thr Asp Ser Thr Glu Ser Lys Asp Asn Arg
            20                  25                  30
Ile Leu Thr Ser Met Gln Ser Ser Ser Leu Asn Arg Asp Asp Ala Pro
        35                  40                  45
Asp Lys Trp Gln Pro Met His Ala Asn Phe Ser Ile Gln Ser Asp Met
    50                  55                  60
Leu Leu Ser Thr Ala Gln Lys Ser Lys Asn Thr Trp Phe Gly Asn Ser
65                  70                  75                  80
Tyr Ile Met Gly Ile Ile Lys Asn Asn Tyr Leu Glu Phe Gly Ala Arg
                85                  90                  95
Phe Glu Asp Leu Tyr Lys Pro Leu Pro Gly His Glu Pro Glu Met Unk
            100                 105                 110
Arg Gly Val Pro His Met Tyr Val Lys Gly Ser Tyr His Trp Ala Glu
        115                 120                 125
Leu Thr Met Gly Asp Phe Tyr Asp Gln Phe Gly Ser Gly Met Val Phe
    130                 135                 140
Arg Thr Tyr Glu Glu Arg Asn Leu Gly Ile Asp Asn Ala Val Arg Gly
145                 150                 155                 160
Gly Arg Ile Val Leu Thr Pro Phe Asp Gly Val Arg Val Lys Gly Ile
                165                 170                 175
Ala Gly Gln Gln Arg Asn Tyr Phe Asp Arg Thr Gly Lys Val Phe Asn
            180                 185                 190
Ser Gly Arg Gly Tyr Leu Leu Gly Ser Asp Leu Glu Leu Asn Val Glu
        195                 200                 205
Arg Trp Ser Ser Ala Met Arg Asp Asn Asp Tyr His Leu Ala Ile Gly
    210                 215                 220
Gly Ser Phe Val Ser Lys His Glu Ala Asp Glu Asp Ile Phe Val Gly
225                 230                 235                 240
Val Gly Glu Asp Arg Lys Arg Leu Asn Leu Pro Leu Asn Val Pro Ile
                245                 250                 255
```

```
Met Gly Leu Arg Thr Asn Phe Gln Lys Gly Gly Leu Ala Leu Tyr Ala
            260                 265                 270
Glu Tyr Gly Tyr Lys Tyr Asn Asp Pro Ser Ala Asp Asn Asp Tyr Ile
        275                 280                 285
Tyr His Asp Gly Gln Ala Ala Leu Leu Ser Ala Ser Tyr Ser Lys Lys
    290                 295                 300
Gly Met Ser Ile Leu Leu Gln Ala Lys Arg Cys Glu Asn Phe Ala Phe
305                 310                 315                 320
Arg Ser Lys Arg Ser Ala Gln Leu Thr Pro Leu Met Ile Asn Tyr Met
                325                 330                 335
Pro Ala Phe Thr Gln Ala His Thr Tyr Thr Leu Ala Ala Ile Tyr Pro
            340                 345                 350
Tyr Ala Thr Gln Pro Gln Gly Glu Trp Ala Phe Gln Gly Glu Leu Arg
        355                 360                 365
Tyr Asn Phe Ala Arg Arg Thr Ala Leu Gly Gly Arg Tyr Gly Thr Gly
    370                 375                 380
Leu Arg Ile Asn Val Ser His Val Arg Gly Leu Asp Lys Lys Met Leu
385                 390                 395                 400
Lys Glu Asn Pro Asp Glu Leu Ile Gly Thr Asp Gly Tyr Thr Val Ser
                405                 410                 415
Phe Phe Gly Met Gly Asp Leu Tyr Tyr Ser Asp Ile Asp Val Glu Ile
            420                 425                 430
Thr Lys Lys Val Ser Pro Gly Phe Asn Phe Thr Leu Thr Tyr Leu Asn
        435                 440                 445
Gln Ile Tyr Asn Asn Lys Val Leu His Gly Ala Ala Gly Glu Lys Pro
    450                 455                 460
Glu Lys Ile Tyr Ala Asn Ile Phe Val Tyr Asp Gly Lys Tyr Lys Leu
465                 470                 475                 480
Ser Asn Lys Val Ala Leu Arg Thr Glu Leu Gln Tyr Leu His Thr Lys
                485                 490                 495
Gln Asp Gln Gly Asp Trp Ile Tyr Gly Met Ala Glu Leu Ser Ile Leu
            500                 505                 510
Pro Ser Leu Met Leu Ser Leu Ser Glu Gln Tyr Asn Ile Gly Glu Thr
        515                 520                 525
Lys Lys His Tyr Val Met Gly Ser Val Thr Tyr Thr His Gly Ala His
    530                 535                 540
```

Arg Val Ala Phe Ser Ala Gly Lys Thr Arg Ala Gly Met Asn Cys Ser
545 550 555 560
Gly Gly Val Cys Arg Val Val Pro Glu Thr Gln Gly Phe Tyr Leu Ser
565 570 575
Tyr Ser Thr Asn Leu
580

(2) INFORMATION FOR SEQ ID NO:125

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 940 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125

Met Asn Lys Phe Tyr Lys Ser Leu Leu Gln Ser Gly Leu Ala Ala Phe
1 5 10 15
Val Ser Met Ala Thr Ala Leu Thr Ala Ser Ala Gln Ile Ser Phe Gly
20 25 30
Gly Glu Pro Leu Ser Phe Ser Ser Arg Ser Ala Gly Thr His Ser Phe
35 40 45
Asp Asp Ala Met Thr Ile Arg Leu Thr Pro Asp Phe Asn Pro Glu Asp
50 55 60
Leu Ile Ala Gln Ser Arg Trp Gln Ser Gln Arg Asp Gly Arg Pro Val

```
65                  70                  75                  80
Arg Ile Gly Gln Val Ile Pro Val Asp Val Asp Phe Ala Ser Lys Ala
                85                  90                  95
Ser His Ile Ser Ser Ile Gly Asp Val Asp Val Tyr Arg Leu Gln Phe
            100                 105                 110
Lys Leu Glu Gly Ala Lys Ala Ile Thr Leu Tyr Tyr Asp Ala Phe Asn
        115                 120                 125
Ile Pro Glu Gly Gly Arg Leu Tyr Ile Tyr Thr Pro Asp His Glu Ile
    130                 135                 140
Val Leu Gly Ala Tyr Thr Asn Ala Thr His Arg Arg Asn Gly Ala Phe
145                 150                 155                 160
Ala Thr Glu Pro Val Pro Gly Ser Glu Leu Ile Met Asp Tyr Glu Val
                165                 170                 175
Ser Arg Gly Gly Thr Leu Pro Asp Ile Lys Ile Ser Gly Ala Gly Tyr
            180                 185                 190
Ile Phe Asp Lys Val Gly Gly Arg Pro Val Thr Asp Asn His Tyr Gly
        195                 200                 205
Ile Gly Glu Asp Asp Ser Asp Ser Asp Cys Glu Ile Asn Ile Asn Cys
    210                 215                 220
Pro Glu Gly Ala Asp Trp Gln Ala Glu Lys Asn Gly Val Val Gln Met
225                 230                 235                 240
Ile Met Val Lys Gly Gln Tyr Ile Ser Met Cys Ser Gly Asn Leu Leu
                245                 250                 255
Asn Asn Thr Lys Gly Asp Phe Thr Pro Leu Ile Ile Ser Ala Gly His
            260                 265                 270
Cys Ala Ser Ile Thr Thr Asn Phe Gly Val Thr Gln Ser Glu Leu Asp
        275                 280                 285
Lys Trp Ile Phe Thr Phe His Tyr Glu Lys Arg Gly Cys Ser Asn Gly
    290                 295                 300
Thr Leu Ala Ile Phe Arg Gly Asn Ser Ile Ile Gly Ala Ser Met Lys
305                 310                 315                 320
Ala Phe Leu Pro Ile Lys Gly Lys Ser Asp Gly Leu Leu Leu Gln Leu
                325                 330                 335
Asn Asp Glu Val Pro Leu Arg Tyr Arg Val Tyr Tyr Asn Gly Trp Asp
            340                 345                 350
Ser Thr Pro Asp Ile Pro Ser Ser Gly Ala Gly Ile His His Pro Ala
```

355 360 365

Gly Asp Ala Met Lys Ile Ser Ile Leu Lys Lys Thr Pro Ala Leu Asn

370 375 380

Thr Trp Ile Ser Ser Ser Gly Ser Gly Gly Thr Asp Asp His Phe Tyr

385 390 395 400

Phe Lys Tyr Asp Gln Gly Gly Thr Glu Gly Gly Ser Ser Gly Ser Ser

405 410 415

Leu Phe Asn Gln Asn Lys His Val Val Gly Thr Leu Thr Gly Gly Ala

420 425 430

Gly Asn Cys Gly Gly Thr Glu Phe Tyr Gly Arg Leu Asn Ser His Trp

435 440 445

Asn Glu Tyr Ala Ser Asp Gly Asn Thr Ser Arg Met Asp Ile Tyr Leu

450 455 460

Asp Pro Gln Asn Asn Gly Gln Thr Thr Ile Leu Asn Gly Thr Tyr Arg

465 470 475 480

Asp Gly Tyr Lys Pro Leu Pro Ser Val Pro Arg Leu Leu Leu Gln Ser

485 490 495

Thr Gly Asp Gln Val Glu Leu Asn Trp Thr Ala Val Pro Ala Asp Gln

500 505 510

Tyr Pro Ser Ser Tyr Gln Val Glu Tyr His Ile Phe Arg Asn Gly Lys

515 520 525

Glu Ile Ala Thr Thr Lys Glu Leu Ser Tyr Ser Asp Ala Ile Asp Glu

530 535 540

Ser Ile Ile Gly Ser Gly Ile Ile Arg Tyr Glu Val Ser Ala Arg Phe

545 550 555 560

Ile Tyr Pro Ser Pro Leu Asp Gly Val Glu Ser Tyr Lys Asp Thr Asp

565 570 575

Lys Thr Ser Ala Asp Leu Ala Ile Gly Asp Ile Gln Thr Lys Leu Lys

580 585 590

Pro Asp Val Thr Pro Leu Pro Gly Gly Gly Val Ser Leu Ser Trp Lys

595 600 605

Val Pro Phe Leu Ser Gln Leu Val Ser Arg Phe Gly Glu Ser Pro Asn

610 615 620

Pro Val Phe Lys Thr Phe Glu Val Pro Tyr Val Ser Ala Ala Ala Ala

625 630 635 640

Gln Thr Pro Asn Pro Pro Val Gly Val Val Ile Ala Asp Lys Phe Met

```
                645                 650                 655
Ala Gly Thr Tyr Pro Glu Lys Ala Ala Ile Ala Ala Val Tyr Val Met
            660                 665                 670
Pro Ser Ala Pro Asp Ser Thr Phe His Leu Phe Leu Lys Ser Asn Thr
        675                 680                 685
Asn Arg Arg Leu Gln Lys Val Thr Thr Pro Ser Asp Trp Gln Ala Gly
    690                 695                 700
Thr Trp Leu Arg Ile Asn Leu Asp Lys Pro Phe Pro Val Asn Asn Asp
705                 710                 715                 720
His Met Leu Phe Ala Gly Ile Arg Met Pro Asn Lys Tyr Lys Leu Asn
                725                 730                 735
Arg Ala Ile Arg Tyr Val Arg Asn Pro Asp Asn Leu Phe Ser Ile Thr
            740                 745                 750
Gly Lys Lys Ile Ser Tyr Asn Asn Gly Val Ser Phe Glu Gly Tyr Gly
        755                 760                 765
Ile Pro Ser Leu Leu Gly Tyr Met Ala Ile Lys Tyr Leu Val Val Asn
    770                 775                 780
Thr Asp Ala Pro Lys Ile Asp Met Ser Leu Val Gln Glu Pro Tyr Ala
785                 790                 795                 800
Lys Gly Thr Asn Val Ala Pro Phe Pro Glu Leu Val Gly Ile Tyr Val
                805                 810                 815
Tyr Lys Asn Gly Thr Phe Ile Gly Thr Gln Asp Pro Ser Val Thr Thr
            820                 825                 830
Tyr Ser Val Ser Asp Gly Thr Glu Ser Asp Glu Tyr Glu Ile Lys Leu
        835                 840                 845
Val Tyr Lys Gly Ser Gly Ile Ser Asn Gly Val Ala Gln Ile Glu Asn
    850                 855                 860
Asn Asn Ala Val Val Ala Tyr Pro Ser Val Val Thr Asp Arg Phe Ser
865                 870                 875                 880
Ile Lys Asn Ala His Met Val His Ala Ala Ala Leu Tyr Ser Leu Asp
                885                 890                 895
Gly Lys Gln Val Arg Ser Trp Asn Asn Leu Arg Asn Gly Val Thr Phe
            900                 905                 910
Ser Val Gln Gly Leu Thr Ala Gly Thr Tyr Met Leu Val Met Gln Thr
        915                 920                 925
Ala Asn Gly Pro Val Ser Gln Lys Ile Val Lys Gln
```

930 935 940

(2) INFORMATION FOR SEQ ID NO:126

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1282 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126

Met Arg Lys Ile Leu Ser Phe Leu Met Met Cys Ser Leu His Leu Gly
1 5 10 15

Leu Gln Ser Gln Thr Trp His Gly Asp Pro Asp Ser Val Ala Ala Leu
20 25 30

Pro Ser Ile Gly Ile Gln Glu Ser Ser Cys Thr Arg Ile Thr Phe Glu
35 40 45

Val Val Phe Pro Gly Phe Tyr Ser Val Glu Lys Arg Glu Gly Asn Gln
50 55 60

Val Phe Gln Arg Ile Ser Met Pro Gly Cys Gly Ser Phe Gly Asn Leu
65 70 75 80

Gly Glu Ala Glu Leu Pro Val Leu Lys Lys Met Ile Ala Val Pro Glu
85 90 95

Phe Ser Thr Ala Asn Val Ala Val Lys Ile Lys Glu Thr Glu Thr Phe
100 105 110

```
Asp Asn Tyr Asn Ile Tyr Pro Asn Pro Thr Tyr Val Val Glu Glu Leu
        115                 120                 125
Pro Glu Gly Gly Thr Tyr Leu Val Glu Ala Phe Ala Ile Asn Asn Asp
    130                 135                 140
Tyr Tyr Ser Gln Asn Val Ser Leu Pro Ser Thr His Tyr Val Tyr Ser
145                 150                 155                 160
Gln Asp Gly Tyr Phe Arg Ser Gln Arg Phe Ile Glu Val Thr Leu Tyr
                165                 170                 175
Pro Phe Arg Tyr Asn Pro Val Arg Gln Glu Ile Leu Phe Ala Lys Lys
            180                 185                 190
Ile Glu Val Thr Ile Thr Phe Asp Asn Pro Gln Pro Pro Leu Gln Lys
        195                 200                 205
Asn Thr Gly Ile Phe Asn Lys Val Ala Ser Ser Ala Phe Ile Asn Tyr
    210                 215                 220
Glu Ala Asp Gly Lys Ser Ala Ile Glu Asn Asp Met Val Phe Ser Arg
225                 230                 235                 240
Gly Thr Thr Thr Tyr Ile Ser Gly Asn Val Ala Ser Asn Leu Pro Gln
                245                 250                 255
Asn Cys Asp Tyr Leu Val Ile Tyr Asp Asp Met Phe Asn Val Asn Gln
            260                 265                 270
Gln Pro His Asp Glu Ile Lys Arg Leu Cys Glu His Arg Ala Phe Tyr
        275                 280                 285
Asn Gly Phe Asp Val Ala Ala Val Ser Ile Lys Asp Val Leu Asn Ser
    290                 295                 300
Phe Pro Ser Asn Ala Thr Ser Tyr Ile Asn Glu Thr Lys Leu Lys Asn
305                 310                 315                 320
Phe Ile Arg Ser Val Tyr Asn Gln Ser Asn Ala Lys Arg Thr Leu Asp
                325                 330                 335
Gly Lys Leu Gly Tyr Val Leu Leu Ile Gly Lys Pro Leu Ser Lys Tyr
            340                 345                 350
Leu Ala Asp Thr Asp Asn Thr Lys Val Pro Thr Ser Phe Ile His Asn
        355                 360                 365
Val Ser Leu Ile Pro Ser His Pro Thr Phe Gly Ser Ile Cys Ala Ser
    370                 375                 380
Asp Tyr Phe Phe Ser Cys Val Ser Pro Leu Asp Thr Val Gly Asp Leu
385                 390                 395                 400
```

```
Phe Ile Gly Arg Phe Ser Val Thr Asn Ala His Glu Leu His Asn Leu
                405                 410                 415
Ile Glu Lys Thr Ile Asn Lys Glu Ile Ser Tyr Asn Pro Ile Ala His
            420                 425                 430
Lys Asn Ile Leu Tyr Ala Glu Gly Lys Gly Cys Asp Ala Pro Ile Leu
        435                 440                 445
Arg Leu Phe Leu Lys Glu Ile Ala Ser Gly Tyr Thr Val Asn Ser Ile
    450                 455                 460
Leu Lys Ser Asn Gln Val Ser Ala Ile Asp Ser Ile Phe Asp Cys Leu
465                 470                 475                 480
Asn Asn Gly Ser His His Phe Tyr Phe Asn Thr His Gly Met Pro Thr
                485                 490                 495
Val Trp Gly Ile Gly Gln Gly Leu Asp Val Asn Thr Leu Thr Ala Arg
            500                 505                 510
Leu Asn Asn Thr Ser Ser Gln Gly Leu Cys Thr Ser Leu Ser Cys Ser
        515                 520                 525
Ser Ala Val Ala Asp Ser Thr Ile Arg Ser Leu Gly Glu Val Leu Thr
    530                 535                 540
Thr Tyr Ala Pro Asn Lys Gly Phe Ser Ala Phe Leu Gly Gly Ser Arg
545                 550                 555                 560
Ala Thr Gln Tyr Ala Val Tyr Leu Glu Gly Pro Cys Pro Pro Ser Glu
                565                 570                 575
Phe Tyr Glu Tyr Leu Pro Tyr Ser Leu Tyr His Asn Leu Ser Thr Val
            580                 585                 590
Val Gly Glu Met Leu Leu Ser Ser Ile Ile Asn Thr Asn Ser Val Asp
        595                 600                 605
Thr Tyr Ser Lys Phe Asn Phe Asn Leu Leu Gly Asp Pro Ala Leu Asn
    610                 615                 620
Ile Met Ala His Gly Met Glu Val Ser Asn Cys Ile Thr Leu Pro Asn
625                 630                 635                 640
Asn Thr Ile Ile Ser Ser Pro Ile Thr Ile Lys Asn Gly Gly Cys Leu
                645                 650                 655
Lys Ile Pro Glu Lys Gly Val Leu His Phe Thr Asn Asn Gly Ser Ile
            660                 665                 670
Gln Val Met Ser Gly Gly Thr Leu Glu Ile Gly Asn Gln Ala Lys Ile
        675                 680                 685
```

```
Ser Gly Glu Thr Gly Ala Asn Pro Thr Phe Ile Thr Val Tyr Gly Asp
    690                 695                 700
Gly Leu Ala Ile Asn Lys Gln Val Glu Ile Asp Asn Ile Asp Arg Leu
705                 710                 715                 720
Asn Leu Phe Ser Thr His Ser Val Met Pro Lys Phe His Phe Asp Ser
                725                 730                 735
Val Lys Phe Asn Ser Ala Pro Leu Tyr Thr Thr Asn Cys Ile Val Glu
            740                 745                 750
Ile Ser Asn Cys Glu Phe Thr Asn Arg Ser Asp Ile Ile Ser Lys Asn
        755                 760                 765
Cys Asp Leu Ser Val Glu Asn Ser Met Phe Ser Ser Ser Gly Ile Thr
    770                 775                 780
Val Phe Lys Pro Met Ala Thr Ser Ser Ile Thr Gly Leu Ser Thr Lys
785                 790                 795                 800
Ala Lys Ile Thr Asp Asn Thr Phe Phe Ala Thr Gly Asn Phe Ala Tyr
                805                 810                 815
His Ile Thr Asn Thr Pro Gly Leu Thr Ala Thr Ser Asn Ala Ala Ile
            820                 825                 830
Lys Leu Asp Asn Ile Pro Glu Tyr Tyr Ile Ser Gly Asn Lys Ile Val
        835                 840                 845
Asn Cys Asp Glu Ala Leu Val Leu Asn Asn Ser Gly Asn Arg Thr Asn
    850                 855                 860
Arg Leu His Asn Ile Thr Arg Asn Val Ile Lys Asn Cys Arg Ile Gly
865                 870                 875                 880
Ser Thr Leu Tyr Asn Ser Tyr Gly Ile Tyr Asn Arg Asn Lys Ile Ser
                885                 890                 895
Asn Asn His Ile Gly Val Arg Leu Leu Asn Asn Ser Cys Phe Tyr Phe
            900                 905                 910
Asp Asn Ala Pro Val Ile Asn Glu Glu Asp Lys Gln Thr Phe Ile Ser
        915                 920                 925
Asn Arg Thr Trp Gln Leu Tyr Ser Ser Asn Gly Thr Phe Pro Leu Asn
    930                 935                 940
Phe His Tyr Asn Ser Leu Gln Gly Gly Asp Thr Asp Thr Trp Ile Tyr
945                 950                 955                 960
Asn Asp Thr Tyr Thr Asn Arg Tyr Ile Asp Val Ser Asn Asn His Trp
                965                 970                 975
```

```
Gly Asn Asn Asp Leu Phe Asp Pro Asn Gln Val Phe Asn Thr Pro Asp
            980                 985                 990
Leu Phe Ile Trp Ile Pro Phe Trp Asp Gly Leu Pro Asn Gly Arg Ser
        995                 1000                1005
Gly Asn Ser Ser Ala Glu Ala Val Glu Phe Gln Thr Ala Leu Asp Cys
    1010                1015                1020
Ile Gly Asn Ser Asp Tyr Leu Ser Ala Lys Val Ala Leu Lys Met Met
1025                1030                1035                1040
Val Glu Thr Tyr Pro Glu Ser Asp Phe Ala Ile Ala Ala Leu Lys Glu
                1045                1050                1055
Leu Phe Arg Ile Glu Lys Met Ser Gly Asn Asp Tyr Glu Gly Leu Lys
            1060                1065                1070
Asp Tyr Phe Arg Ser Asn Pro Thr Ile Ile Ser Ser Gln Asn Leu Phe
        1075                1080                1085
Pro Thr Ala Asp Phe Leu Ser Ala Arg Cys Asp Ile Val Cys Glu Asn
    1090                1095                1100
Tyr Gln Ser Ala Ile Asp Trp Tyr Glu Asn Arg Leu Asn Ser Glu Ile
1105                1110                1115                1120
Ser Tyr Gln Asp Ser Val Phe Ala Val Ile Asp Leu Gly Asp Ile Tyr
                1125                1130                1135
Trp Asn Met Gln Leu Asp Ser Leu Arg Gly Thr Gly Ile Asp Leu Asn
            1140                1145                1150
Ile Leu Ser Cys Glu Gln Arg Lys Ser Leu Glu Ser His Gln Asn Val
        1155                1160                1165
Lys Asn Tyr Leu Leu Ser Thr Leu Pro Glu Ser Thr Gly Thr Leu Leu
    1170                1175                1180
Pro Pro Leu Glu Cys Asn Lys Ser Ser Leu Asp Lys Ser Lys Ile Ile
1185                1190                1195                1200
Ser Ile Ser Pro Asn Pro Ala Lys Ala Val Val Thr Ile Ile Tyr Tyr
                1205                1210                1215
Thr Asp Asn Pro Ser Cys Ser Val Ile Lys Ile Tyr Gly Ile Asn Gly
            1220                1225                1230
Ala Ser Ala Asp Ile Thr Gly Leu Pro Lys His Leu Ser Glu Gly Tyr
        1235                1240                1245
Tyr Ser Ile Gln Phe Asn Thr Ser Asn Phe Asp Pro Gly Phe Tyr Leu
    1250                1255                1260
```

Val Thr Leu Asn Val Asp Gln Lys Ile Ile Asp Thr Glu Lys Leu Arg
1265 1270 1275 1280
Ile Lys

(2) INFORMATION FOR SEQ ID NO:127

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 925 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127

Met Ala Ile Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile
1 5 10 15
Leu Leu Ser Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser
20 25 30
Gly Met Asn Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile
35 40 45
Leu Tyr Glu Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu
50 55 60
Ile Asp Ala Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser
65 70 75 80
Phe Ser Val Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile

85 90 95

Arg Ser Gly Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile

100 105 110

Glu Gly Ala Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr

115 120 125

Asn Pro Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile

130 135 140

Glu Asp Phe Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr

145 150 155 160

Pro Leu Val Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys

165 170 175

Tyr Ile Ala Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe

180 185 190

Leu Lys Leu Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu

195 200 205

Pro Ala Thr Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg

210 215 220

Leu Thr Trp Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn

225 230 235 240

Glu Glu Leu Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu

245 250 255

Leu Ala Gln Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr

260 265 270

Tyr Ser Leu Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala

275 280 285

Val Tyr Asp Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His

290 295 300

Tyr Ala Thr Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val

305 310 315 320

Pro Asn Gly Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp

325 330 335

Gly His Tyr Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly

340 345 350

His Cys Ser Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr

355 360 365

Pro Asp Asn Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val

```
    370                 375                 380
Lys Tyr Trp Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr
385                 390                 395                 400
Ala Val Met Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile
                405                 410                 415
Leu Phe Glu Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu
            420                 425                 430
Arg Thr Ile Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His
        435                 440                 445
Tyr Asn Cys Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val
    450                 455                 460
Phe Gly Thr Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val
465                 470                 475                 480
Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn
                485                 490                 495
Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala
            500                 505                 510
Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp
        515                 520                 525
Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp
    530                 535                 540
Gln Val Glu Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile
545                 550                 555                 560
Glu Ser Gln Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp
                565                 570                 575
Ile Ile Leu Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp
            580                 585                 590
Leu Leu Ile Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro
        595                 600                 605
Trp Thr Met Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser
    610                 615                 620
Tyr Leu Pro Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr
625                 630                 635                 640
Pro Arg Leu Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln
                645                 650                 655
Asp Ala Val Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr
```

660 665 670

Gly Thr Ala Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr

675 680 685

Ala Lys Ala Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala

690 695 700

Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe

705 710 715 720

Phe Leu Leu Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val

725 730 735

Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys

740 745 750

Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr

755 760 765

Asp Asp Lys Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn

770 775 780

Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile

785 790 795 800

Asp Glu Thr Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys

805 810 815

Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp

820 825 830

Lys Leu Asn Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr

835 840 845

Ser Leu Lys Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu

850 855 860

Gly Leu Ser Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly

865 870 875 880

Ile Cys Ile Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp

885 890 895

Val Ser Arg Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly

900 905 910

Asn Lys Thr Thr Thr Glu Lys Val Glu Ile Lys Arg Pro

915 920 925

(2) INFORMATION FOR SEQ ID NO:128

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 922 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128

```
Met Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser
1               5                   10                  15
Trp Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn
            20                  25                  30
Ala Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu
        35                  40                  45
Ser Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala
    50                  55                  60
Asp Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val
65                  70                  75                  80
Pro Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly
                85                  90                  95
Ile Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala
            100                 105                 110
Lys Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu
        115                 120                 125
His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe
    130                 135                 140
```

```
Val Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val
145                 150                 155                 160
Trp Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala
                165                 170                 175
Trp Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu
            180                 185                 190
Asp Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr
        195                 200                 205
Asp Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp
    210                 215                 220
Asn Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu
225                 230                 235                 240
Gln Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln
                245                 250                 255
Ile Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu
            260                 265                 270
Arg Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp
        275                 280                 285
Glu Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr
    290                 295                 300
Asp Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly
305                 310                 315                 320
Trp Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr
                325                 330                 335
Leu Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser
            340                 345                 350
Leu Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn
        355                 360                 365
Tyr Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp
    370                 375                 380
Val Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met
385                 390                 395                 400
Ala Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu
                405                 410                 415
Glu Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile
            420                 425                 430
```

```
Asn Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys
        435                 440                 445
Thr Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr
    450                 455                 460
Pro Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile
465                 470                 475                 480
Glu Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu
                485                 490                 495
Pro Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala Gly Tyr Asn
            500                 505                 510
Ile Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val
        515                 520                 525
Leu Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp Gln Val Glu
    530                 535                 540
Val Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln
545                 550                 555                 560
Ser Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp Ile Ile Leu
                565                 570                 575
Tyr Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp Leu Leu Ile
            580                 585                 590
Asp Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro Trp Thr Met
        595                 600                 605
Tyr Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser Tyr Leu Pro
    610                 615                 620
Met Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr Pro Arg Leu
625                 630                 635                 640
Glu Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val
                645                 650                 655
Tyr Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala
            660                 665                 670
Val Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala
        675                 680                 685
Asn Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys
    690                 695                 700
Tyr Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu
705                 710                 715                 720
```

Leu Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro
725 730 735

Val Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu
740 745 750

Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys
755 760 765

Lys Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu
770 775 780

Leu Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr
785 790 795 800

Tyr Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala
805 810 815

Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn
820 825 830

Tyr Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys
835 840 845

Ile Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser
850 855 860

Arg Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile
865 870 875 880

Leu Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg
885 890 895

Leu Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr
900 905 910

Thr Thr Glu Lys Val Glu Ile Lys Arg Pro
915 920

(2) INFORMATION FOR SEQ ID NO:129

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 921 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...921

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129

```
Met Lys Ser Ile Val Phe Arg Ala Phe Leu Thr Ile Leu Leu Ser Trp
1               5                   10                  15
Ala Ala Ile Thr Asn Pro Thr Ala Gln Glu Ile Ser Gly Met Asn Ala
            20                  25                  30
Ser Cys Leu Ala Ala Pro Ala Gln Pro Asp Thr Ile Leu Tyr Glu Ser
        35                  40                  45
Phe Glu Asn Gly Pro Val Pro Asn Gly Trp Leu Glu Ile Asp Ala Asp
    50                  55                  60
Ala Asp Gly Ala Thr Trp Gly Ser Pro Ser Gly Ser Phe Ser Val Pro
65                  70                  75                  80
Tyr Gly His Asn Gly Leu Cys Thr Tyr Ser His Ile Arg Ser Gly Ile
                85                  90                  95
Ser Thr Ala Gly Asn Tyr Leu Ile Thr Pro Asn Ile Glu Gly Ala Lys
            100                 105                 110
Arg Val Lys Tyr Trp Val Cys Asn Gln Tyr Ser Thr Asn Pro Glu His
        115                 120                 125
Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Ile Glu Asp Phe Val
    130                 135                 140
Leu Leu Phe Asp Asp Ser Ile Thr Gly Lys Pro Thr Pro Leu Val Trp
145                 150                 155                 160
Arg Arg Arg Ile Val Asp Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp
                165                 170                 175
Arg His Tyr Lys Val Thr Asp Ser His Thr Glu Phe Leu Lys Leu Asp
            180                 185                 190
Asp Val Thr Val Tyr Arg Ser Ile Glu Gly Pro Glu Pro Ala Thr Asp
```

```
        195                 200                 205
Phe Thr Val Ile Asn Ile Gly Gln Asn Val Gly Arg Leu Thr Trp Asn
    210                 215                 220
Tyr Pro Glu Asp Tyr Gln Pro Glu Gly Lys Gly Asn Glu Glu Leu Gln
225                 230                 235                 240
Leu Ser Gly Tyr Asn Ile Tyr Ala Asn Gly Thr Leu Leu Ala Gln Ile
                245                 250                 255
Lys Asp Val Ser Ile Leu Glu Tyr Val Asp Ser Thr Tyr Ser Leu Arg
            260                 265                 270
Asp Asn Pro Leu Gln Val Glu Tyr Cys Val Thr Ala Val Tyr Asp Glu
        275                 280                 285
Ser Ile Glu Ser Ser Thr Val Cys Gly Thr Leu His Tyr Ala Thr Asp
    290                 295                 300
Ala Ile Leu Tyr Glu Asn Phe Glu Asn Gly Pro Val Pro Asn Gly Trp
305                 310                 315                 320
Leu Val Ile Asp Ala Asp Gly Asp Gly Phe Ser Trp Gly His Tyr Leu
                325                 330                 335
Asn Ala Tyr Asp Ala Phe Pro Gly His Asn Gly Gly His Cys Ser Leu
            340                 345                 350
Ser Ala Ser Tyr Val Pro Gly Ile Gly Pro Val Thr Pro Asp Asn Tyr
        355                 360                 365
Leu Ile Thr Pro Lys Val Glu Gly Ala Lys Arg Val Lys Tyr Trp Val
    370                 375                 380
Ser Thr Gln Asp Ala Asn Trp Ala Ala Glu His Tyr Ala Val Met Ala
385                 390                 395                 400
Ser Thr Thr Gly Thr Ala Val Gly Asp Phe Val Ile Leu Phe Glu Glu
                405                 410                 415
Thr Met Thr Ala Lys Pro Thr Gly Ala Trp Tyr Glu Arg Thr Ile Asn
            420                 425                 430
Leu Pro Glu Gly Thr Lys Tyr Ile Ala Trp Arg His Tyr Asn Cys Thr
        435                 440                 445
Asp Ile Tyr Phe Leu Lys Leu Asp Asp Ile Thr Val Phe Gly Thr Pro
    450                 455                 460
Ala Ser Glu Pro Glu Pro Val Thr Asp Phe Val Val Ser Leu Ile Glu
465                 470                 475                 480
Asn Asn Lys Gly Arg Leu Lys Trp Asn Tyr Pro Asn Gly Tyr Glu Pro
```

```
                485                 490                 495
Asp Lys Thr Asp Asp Lys Asp Pro Leu Gln Leu Ala Gly Tyr Asn Ile
            500                 505                 510
Tyr Ala Asn Gly Ser Leu Leu Val His Ile Gln Asp Pro Thr Val Leu
        515                 520                 525
Glu Tyr Ile Asp Glu Thr Tyr Ser Ser Arg Asp Asp Gln Val Glu Val
    530                 535                 540
Glu Tyr Cys Val Thr Ala Val Tyr Asn Asp Asn Ile Glu Ser Gln Ser
545                 550                 555                 560
Val Cys Asp Lys Leu Ile Tyr Asp Ser Gln Ser Asp Ile Ile Leu Tyr
                565                 570                 575
Glu Gly Phe Glu Ala Gly Ser Ile Pro Glu Gly Trp Leu Leu Ile Asp
            580                 585                 590
Ala Asp Gly Asp Asn Val Asn Trp Asp Tyr Tyr Pro Trp Thr Met Tyr
        595                 600                 605
Gly His Asp Ser Glu Lys Cys Ile Ala Ser Pro Ser Tyr Leu Pro Met
    610                 615                 620
Ile Gly Val Leu Thr Pro Asp Asn Tyr Leu Val Thr Pro Arg Leu Glu
625                 630                 635                 640
Gly Ala Lys Leu Val Lys Tyr Trp Val Ser Ala Gln Asp Ala Val Tyr
                645                 650                 655
Ser Ala Glu His Tyr Ala Val Met Val Ser Thr Thr Gly Thr Ala Val
            660                 665                 670
Glu Asp Phe Val Leu Leu Phe Glu Glu Thr Met Thr Ala Lys Ala Asn
        675                 680                 685
Gly Ala Trp Tyr Glu Arg Thr Ile Thr Leu Pro Ala Gly Thr Lys Tyr
    690                 695                 700
Ile Ala Trp Arg His Tyr Asp Cys Thr Asp Met Phe Phe Leu Leu Leu
705                 710                 715                 720
Asp Asp Ile Thr Val Tyr Arg Ser Thr Glu Thr Val Pro Glu Pro Val
                725                 730                 735
Thr Asp Phe Val Val Ser Leu Ile Glu Asn Asn Lys Gly Arg Leu Lys
            740                 745                 750
Trp Asn Tyr Pro Asn Gly Tyr Glu Pro Asp Lys Thr Asp Asp Lys Lys
        755                 760                 765
Pro Leu Gln Leu Thr Gly Tyr Asn Ile Tyr Ala Asn Gly Ser Leu Leu
```

```
    770                     775                     780
Val His Ile Gln Asp Pro Thr Val Leu Glu Tyr Ile Asp Glu Thr Tyr
785                 790                     795                 800
Ser Ser Arg Asp Gly Gln Val Glu Met Glu Tyr Cys Val Thr Ala Val
                805                     810                     815
Tyr Asn Asp Asn Ile Glu Ser Gln Ser Val Cys Asp Lys Leu Asn Tyr
            820                     825                     830
Thr Ile Thr Ser Leu Asp Asn Ile Gln Ser Asp Thr Ser Leu Lys Ile
        835                     840                     845
Tyr Pro Asn Pro Ala Ser Tyr Val Val Arg Ile Glu Gly Leu Ser Arg
    850                     855                     860
Ser Lys Ser Thr Ile Glu Leu Tyr Asn Ala Leu Gly Ile Cys Ile Leu
865                 870                     875                 880
Arg Glu Glu Thr His Ser Glu Lys Thr Glu Ile Asp Val Ser Arg Leu
                885                     890                     895
Asn Asp Gly Val Tyr Leu Ile Lys Val Val Gly Gly Asn Lys Thr Thr
            900                     905                     910
Thr Glu Lys Val Glu Ile Lys Arg Pro
        915                     920
```

(2) INFORMATION FOR SEQ ID NO:130

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 1226 amino acids
  (B) TYPE: amino acid
  (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
  (A) NAME/KEY: misc_feature

(B) LOCATION 1...1226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130

```
Met Met Lys Arg Tyr Thr Ile Ile Leu Ala Val Phe Leu Leu Phe Cys
1               5                   10                  15
Thr Val Phe Thr Phe Gln Ile Lys Ala Arg Pro Tyr Glu Arg Phe Ala
            20                  25                  30
Asp Val Glu Lys Pro Trp Ile Gln Lys His Ser Met Asp Ser Lys Leu
        35                  40                  45
Val Pro Ala Asn Lys Gly Asn Leu Ile Gln Ala Glu Ile Val Tyr Gln
    50                  55                  60
Ser Val Ser Glu His Ser Asp Leu Val Ile Ser Pro Val Asn Glu Ile
65                  70                  75                  80
Arg Pro Ala Asn Arg Phe Pro Ser His Arg Lys Ser Phe Phe Ala Glu
                85                  90                  95
Asn Leu Arg Ala Ser Pro Pro Val Val Pro Val Ala Val Asp Lys Tyr
            100                 105                 110
Ala Val Pro Val Ala Asn Pro Met Asp Pro Glu Asn Pro Asn Ala Trp
        115                 120                 125
Asp Val Thr Leu Lys Ile Thr Thr Lys Ala Val Thr Val Pro Val Asp
    130                 135                 140
Val Val Met Val Ile Asp Gln Ser Ser Ser Met Gly Gly Gln Asn Ile
145                 150                 155                 160
Ala Arg Leu Lys Ser Ala Ile Ala Ser Gly Gln Arg Phe Val Lys Lys
                165                 170                 175
Met Leu Pro Lys Gly Thr Ala Thr Glu Gly Val Arg Ile Ala Leu Val
            180                 185                 190
Ser Tyr Asp His Glu Pro His Arg Leu Ser Asp Phe Thr Lys Asp Thr
        195                 200                 205
Ala Phe Leu Cys Gln Lys Ile Arg Ala Leu Thr Pro Ile Trp Gly Thr
    210                 215                 220
His Thr Gln Gly Gly Leu Lys Met Ala Arg Asn Ile Met Ala Thr Ser
225                 230                 235                 240
Thr Ala Val Asp Lys His Ile Ile Leu Met Ser Asp Gly Leu Ala Thr
                245                 250                 255
```

```
Glu Gln Tyr Pro Val Lys Asn Val Thr Thr Ala Asp Phe Ile Gly Lys
            260                 265                 270
Thr Gly Asn Ala Asn Asp Pro Ile Asp Leu Val Ile Gln Gly Ala Ile
        275                 280                 285
Asn Phe Pro Thr Asn Tyr Val Ser Asn Asn Pro Ser Thr Pro Leu Thr
    290                 295                 300
Pro Asn Tyr Pro Thr His Ser Ser Lys Val Gly Arg Arg Asn Leu Pro
305                 310                 315                 320
Glu Ser Lys Phe Asp Tyr Ser Asn Leu Ser Ala Arg Ile Thr Phe Asp
                325                 330                 335
Gly Val Ala Gly Ala Leu Val Tyr Glu Pro Arg Phe Pro His Pro Tyr
            340                 345                 350
Tyr Tyr Tyr Phe Pro Cys Asn Ala Ala Ile Asn Glu Ala Gln Phe Ala
        355                 360                 365
Lys Asn Ser Gly Tyr Thr Ile His Thr Ile Gly Tyr Asp Leu Gly Asp
    370                 375                 380
Phe Ala Leu Ala Asn Asn Ser Leu Lys Leu Thr Ala Thr Asp Glu Asn
385                 390                 395                 400
His Phe Phe Thr Ala Thr Pro Ala Asn Leu Ala Ala Ala Phe Asp Asn
                405                 410                 415
Ile Ala Gln Thr Ile Asn Ile Gly Ile Gln Arg Gly Glu Val Thr Asp
            420                 425                 430
Phe Val Ala Pro Gly Phe Ile Val Lys Asn Leu Thr Gln Ser Gly Asp
        435                 440                 445
Val Thr His Leu Leu Asn Val Ser Asn Gly Thr Val His Tyr Asp Val
    450                 455                 460
Ser Thr Lys Lys Leu Thr Trp Thr Thr Gly Thr Ile Leu Ser Ser Ser
465                 470                 475                 480
Glu Ala Thr Ile Thr Tyr Arg Ile Tyr Ala Asp Leu Asp Tyr Ile Gln
                485                 490                 495
Asn Asn Asp Ile Pro Val Asn Thr Thr Ser Ala Ile Gly Pro Asp Leu
            500                 505                 510
Gly Gly Phe Asp Thr Asn Thr Glu Ala Lys Leu Thr Tyr Thr Asn Ser
        515                 520                 525
Asn Gly Glu Pro Asn Gln Gln Leu Ile Phe Pro Arg Pro Thr Val Lys
    530                 535                 540
```

```
Leu Gly Tyr Gly Val Ile Lys Arg His Tyr Val Leu Val Asn Lys Asp
545                 550                 555                 560
Gly Gln Pro Ile Gln Ala Asn Gly Thr Val Val Ser Ser Leu Ser Glu
                565                 570                 575
Ala His Val Leu Gln Ser Gln Asp Phe Phe Leu Pro Ser Gly Gly Gly
            580                 585                 590
His Ile Val Pro Lys Trp Ile Lys Leu Asp Lys Thr Thr Glu Ala Leu
        595                 600                 605
Gln Tyr Tyr Ser Val Pro Pro Thr Asn Thr Val Ile Thr Thr Ala Asp
    610                 615                 620
Gly Lys Arg Tyr Arg Phe Val Glu Val Pro Gly Ser Thr Pro Asn Pro
625                 630                 635                 640
Gly Gln Ile Gly Ile Ser Trp Lys Lys Pro Ala Gly Asn Ala Tyr Phe
                645                 650                 655
Ala Tyr Lys Leu Leu Asn Tyr Trp Met Gly Gly Thr Thr Asp Gln Gln
            660                 665                 670
Ser Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu
        675                 680                 685
Thr Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro
    690                 695                 700
Ala Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly
705                 710                 715                 720
Asn Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser
                725                 730                 735
Gln Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly
            740                 745                 750
Thr Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu
        755                 760                 765
Phe Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe
    770                 775                 780
Tyr Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser
785                 790                 795                 800
Trp Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn
                805                 810                 815
Asp Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn
            820                 825                 830
```

Gly Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln
835 840 845

Lys Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr
850 855 860

Gly Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu
865 870 875 880

Asn Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile
885 890 895

Gly Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe
900 905 910

Pro Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg
915 920 925

Asp Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala
930 935 940

Gly Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu
945 950 955 960

Pro Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn
965 970 975

Gly Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn
980 985 990

Thr Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly
995 1000 1005

Asn Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly
1010 1015 1020

Asn Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser
1025 1030 1035 1040

Phe Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly
1045 1050 1055

Leu Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln
1060 1065 1070

Val Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala
1075 1080 1085

Asp Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe
1090 1095 1100

Ala Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His
1105 1110 1115 1120

```
Arg Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp
                1125                1130                1135
Ser Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp
            1140                1145                1150
Asp Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn
        1155                1160                1165
Gln Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys
    1170                1175                1180
Leu Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys
1185                1190                1195                1200
Val Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr
                1205                1210                1215
Asn Asp Val His Lys Val Leu Val Glu Tyr
            1220                1225
```

(2) INFORMATION FOR SEQ ID NO:131

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1225 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...1225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131

```
Met Lys Arg Tyr Thr Ile Ile Leu Ala Val Phe Leu Leu Phe Cys Thr
```

```
1               5                   10                  15
Val Phe Thr Phe Gln Ile Lys Ala Arg Pro Tyr Glu Arg Phe Ala Asp
            20                  25                  30
Val Glu Lys Pro Trp Ile Gln Lys His Ser Met Asp Ser Lys Leu Val
        35                  40                  45
Pro Ala Asn Lys Gly Asn Leu Ile Gln Ala Glu Ile Val Tyr Gln Ser
    50                  55                  60
Val Ser Glu His Ser Asp Leu Val Ile Ser Pro Val Asn Glu Ile Arg
65                  70                  75                  80
Pro Ala Asn Arg Phe Pro Ser His Arg Lys Ser Phe Phe Ala Glu Asn
                85                  90                  95
Leu Arg Ala Ser Pro Pro Val Val Pro Val Ala Val Asp Lys Tyr Ala
            100                 105                 110
Val Pro Val Ala Asn Pro Met Asp Pro Glu Asn Pro Asn Ala Trp Asp
        115                 120                 125
Val Thr Leu Lys Ile Thr Thr Lys Ala Val Thr Val Pro Val Asp Val
    130                 135                 140
Val Met Val Ile Asp Gln Ser Ser Ser Met Gly Gly Gln Asn Ile Ala
145                 150                 155                 160
Arg Leu Lys Ser Ala Ile Ala Ser Gly Gln Arg Phe Val Lys Lys Met
                165                 170                 175
Leu Pro Lys Gly Thr Ala Thr Glu Gly Val Arg Ile Ala Leu Val Ser
            180                 185                 190
Tyr Asp His Glu Pro His Arg Leu Ser Asp Phe Thr Lys Asp Thr Ala
        195                 200                 205
Phe Leu Cys Gln Lys Ile Arg Ala Leu Thr Pro Ile Trp Gly Thr His
    210                 215                 220
Thr Gln Gly Gly Leu Lys Met Ala Arg Asn Ile Met Ala Thr Ser Thr
225                 230                 235                 240
Ala Val Asp Lys His Ile Ile Leu Met Ser Asp Gly Leu Ala Thr Glu
                245                 250                 255
Gln Tyr Pro Val Lys Asn Val Thr Thr Ala Asp Phe Ile Gly Lys Thr
            260                 265                 270
Gly Asn Ala Asn Asp Pro Ile Asp Leu Val Ile Gln Gly Ala Ile Asn
        275                 280                 285
Phe Pro Thr Asn Tyr Val Ser Asn Asn Pro Ser Thr Pro Leu Thr Pro
```

```
    290                 295                 300
Asn Tyr Pro Thr His Ser Ser Lys Val Gly Arg Arg Asn Leu Pro Glu
305                 310                 315                 320
Ser Lys Phe Asp Tyr Ser Asn Leu Ser Ala Arg Ile Thr Phe Asp Gly
                325                 330                 335
Val Ala Gly Ala Leu Val Tyr Glu Pro Arg Phe Pro His Pro Tyr Tyr
            340                 345                 350
Tyr Tyr Phe Pro Cys Asn Ala Ala Ile Asn Glu Ala Gln Phe Ala Lys
        355                 360                 365
Asn Ser Gly Tyr Thr Ile His Thr Ile Gly Tyr Asp Leu Gly Asp Phe
    370                 375                 380
Ala Leu Ala Asn Asn Ser Leu Lys Leu Thr Ala Thr Asp Glu Asn His
385                 390                 395                 400
Phe Phe Thr Ala Thr Pro Ala Asn Leu Ala Ala Ala Phe Asp Asn Ile
                405                 410                 415
Ala Gln Thr Ile Asn Ile Gly Ile Gln Arg Gly Glu Val Thr Asp Phe
            420                 425                 430
Val Ala Pro Gly Phe Ile Val Lys Asn Leu Thr Gln Ser Gly Asp Val
        435                 440                 445
Thr His Leu Leu Asn Val Ser Asn Gly Thr Val His Tyr Asp Val Ser
    450                 455                 460
Thr Lys Lys Leu Thr Trp Thr Thr Gly Thr Ile Leu Ser Ser Ser Glu
465                 470                 475                 480
Ala Thr Ile Thr Tyr Arg Ile Tyr Ala Asp Leu Asp Tyr Ile Gln Asn
                485                 490                 495
Asn Asp Ile Pro Val Asn Thr Thr Ser Ala Ile Gly Pro Asp Leu Gly
            500                 505                 510
Gly Phe Asp Thr Asn Thr Glu Ala Lys Leu Thr Tyr Thr Asn Ser Asn
        515                 520                 525
Gly Glu Pro Asn Gln Gln Leu Ile Phe Pro Arg Pro Thr Val Lys Leu
    530                 535                 540
Gly Tyr Gly Val Ile Lys Arg His Tyr Val Leu Val Asn Lys Asp Gly
545                 550                 555                 560
Gln Pro Ile Gln Ala Asn Gly Thr Val Val Ser Ser Leu Ser Glu Ala
                565                 570                 575
His Val Leu Gln Ser Gln Asp Phe Phe Leu Pro Ser Gly Gly Gly His
```

```
            580                 585                 590
Ile Val Pro Lys Trp Ile Lys Leu Asp Lys Thr Thr Glu Ala Leu Gln
        595                 600                 605
Tyr Tyr Ser Val Pro Pro Thr Asn Thr Val Ile Thr Thr Ala Asp Gly
    610                 615                 620
Lys Arg Tyr Arg Phe Val Glu Val Pro Gly Ser Thr Pro Asn Pro Gly
625                 630                 635                 640
Gln Ile Gly Ile Ser Trp Lys Lys Pro Ala Gly Asn Ala Tyr Phe Ala
                645                 650                 655
Tyr Lys Leu Leu Asn Tyr Trp Met Gly Gly Thr Thr Asp Gln Gln Ser
            660                 665                 670
Glu Trp Asp Val Thr Ser Asn Trp Thr Gly Ala Gln Val Pro Leu Thr
        675                 680                 685
Gly Glu Asp Val Glu Phe Ala Thr Thr Glu Asn Phe Gly Ser Pro Ala
    690                 695                 700
Val Ala Asp Leu His Val Pro Thr Thr Asn Pro Lys Ile Ile Gly Asn
705                 710                 715                 720
Leu Ile Asn Asn Ser Asp Lys Asp Leu Val Val Thr Thr Ser Ser Gln
                725                 730                 735
Leu Thr Ile Asn Gly Val Val Glu Asp Asn Asn Pro Asn Val Gly Thr
            740                 745                 750
Ile Val Val Lys Ser Ser Lys Asp Asn Pro Thr Gly Thr Leu Leu Phe
        755                 760                 765
Ala Asn Pro Gly Tyr Asn Gln Asn Val Gly Gly Thr Val Glu Phe Tyr
    770                 775                 780
Asn Gln Gly Tyr Asp Cys Ala Asp Cys Gly Met Tyr Arg Arg Ser Trp
785                 790                 795                 800
Gln Tyr Phe Gly Ile Pro Val Asn Glu Ser Gly Phe Pro Ile Asn Asp
                805                 810                 815
Val Gly Gly Asn Glu Thr Val Asn Gln Trp Val Glu Pro Phe Asn Gly
            820                 825                 830
Asp Lys Trp Arg Pro Ala Pro Tyr Ala Pro Asp Thr Glu Leu Gln Lys
        835                 840                 845
Phe Lys Gly Tyr Gln Ile Thr Asn Asp Val Gln Ala Gln Pro Thr Gly
    850                 855                 860
Val Tyr Ser Phe Lys Gly Met Ile Cys Val Cys Asp Ala Phe Leu Asn
```

```
865                 870                 875                 880
Leu Thr Arg Thr Ser Gly Val Asn Tyr Ser Gly Ala Asn Leu Ile Gly
                885                 890                 895
Asn Ser Tyr Thr Gly Ala Ile Asp Ile Lys Gln Gly Ile Val Phe Pro
            900                 905                 910
Pro Glu Val Glu Gln Thr Val Tyr Leu Phe Asn Thr Gly Thr Arg Asp
        915                 920                 925
Gln Trp Arg Lys Leu Asn Gly Ser Thr Val Ser Gly Tyr Arg Ala Gly
    930                 935                 940
Gln Tyr Leu Ser Val Pro Lys Asn Thr Ala Gly Gln Asp Asn Leu Pro
945                 950                 955                 960
Asp Arg Ile Pro Ser Met His Ser Phe Leu Val Lys Met Gln Asn Gly
                965                 970                 975
Ala Ser Cys Thr Leu Unk Ile Leu Tyr Asp Lys Leu Leu Lys Asn Thr
            980                 985                 990
Thr Val Asn Asn Gly Asn Gly Thr Gln Ile Thr Trp Arg Ser Gly Asn
        995                 1000                1005
Ser Gly Ser Ala Asn Met Pro Ser Leu Val Met Asp Val Leu Gly Asn
    1010                1015                1020
Glu Ser Ala Asp Arg Leu Trp Ile Phe Thr Asp Gly Gly Leu Ser Phe
1025                1030                1035                1040
Gly Phe Asp Asn Gly Trp Asp Gly Arg Lys Leu Thr Glu Lys Gly Leu
                1045                1050                1055
Ser Gln Leu Tyr Ala Met Ser Asp Ile Gly Asn Asp Lys Phe Gln Val
            1060                1065                1070
Ala Gly Val Pro Glu Leu Asn Asn Leu Leu Ile Gly Phe Asp Ala Asp
        1075                1080                1085
Lys Asp Gly Gln Tyr Thr Leu Glu Phe Ala Leu Ser Asp His Phe Ala
    1090                1095                1100
Lys Gly Ala Val Tyr Leu His Asp Leu Gln Ser Gly Ala Lys His Arg
1105                1110                1115                1120
Ile Thr Asn Ser Thr Ser Tyr Ser Phe Asp Ala Lys Arg Gly Asp Ser
                1125                1130                1135
Gly Ala Arg Phe Arg Leu Ser Tyr Gly Cys Asp Glu Asn Val Asp Asp
            1140                1145                1150
Ser His Val Val Ser Thr Asn Gly Arg Glu Ile Ile Ile Leu Asn Gln
```

1155 1160 1165

Asp Ala Leu Asp Cys Thr Val Thr Leu Phe Thr Ile Glu Gly Lys Leu

1170 1175 1180

Leu Arg Arg Leu Lys Val Leu Ala Gly His Arg Glu Val Met Lys Val

1185 1190 1195 1200

Gln Thr Gly Gly Ala Tyr Ile Val His Leu Gln Asn Ala Phe Thr Asn

1205 1210 1215

Asp Val His Lys Val Leu Val Glu Tyr

1220 1225

(2) INFORMATION FOR SEQ ID NO:132

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132

Met Glu Val Lys Lys Asn Thr Val Val Leu Arg Leu Leu Ile Trp Phe

1 5 10 15

Val Ala Ile Leu Leu Phe His Ser Ser Arg Leu Trp Gly Gln Glu Gly

20 25 30

Glu Gly Ser Ala Arg Tyr Arg Phe Lys Gly Phe Val Asp Thr Tyr His

35 40 45

```
Ala Val Arg Ser Ser Ser Pro Phe Asp Phe Met Ser Ser Arg Thr Arg
    50                  55                  60
Val Arg Gly Glu Leu Glu Arg Ser Phe Gly Asn Ser Lys Val Ala Val
65                  70                  75                  80
Ser Val Asn Ala Thr Tyr Asn Ala Leu Leu Lys Asp Glu Thr Gly Leu
                85                  90                  95
Arg Leu Arg Glu Ala Phe Phe Glu His Gln Glu Glu His Trp Gly Leu
            100                 105                 110
Arg Leu Gly Arg Gln Ile Val Ile Trp Gly Ala Ala Asp Gly Val Arg
        115                 120                 125
Ile Thr Asp Leu Ile Ser Pro Met Asp Met Thr Glu Phe Leu Ala Gln
    130                 135                 140
Asp Tyr Asp Asp Ile Arg Met Pro Val Asn Ala Leu Arg Phe Ser Val
145                 150                 155                 160
Phe Asn Glu Ser Met Lys Val Glu Val Val Val Leu Pro Val Phe Glu
                165                 170                 175
Gly Tyr Arg Leu Pro Val Asp Pro Arg Asn Pro Trp Asn Ile Phe Ser
            180                 185                 190
Leu Ser Pro Ile Ala Gln Gly Met Asn Ile Val Trp Lys Glu Glu Ala
        195                 200                 205
Gly Lys Pro Ala Phe Lys Val Ala Asn Ile Glu Tyr Gly Ala Arg Trp
    210                 215                 220
Ser Thr Thr Leu Ser Gly Ile Asp Phe Ala Leu Ala Ala Leu His Thr
225                 230                 235                 240
Trp Asn Lys Met Pro Val Ile Glu Val Gln Gly Ile Val Pro Thr Glu
                245                 250                 255
Ile Ile Val Ser Pro Arg Tyr Tyr Arg Met Gly Phe Val Gly Gly Asp
            260                 265                 270
Leu Ser Val Pro Val Gly Gln Phe Val Phe Arg Gly Glu Ala Ala Phe
        275                 280                 285
Asn Ile Asp Lys His Phe Thr Tyr Lys Ser His Ala Glu Gln Glu Gly
    290                 295                 300
Phe Gln Thr Ile Asn Trp Leu Ala Gly Ala Asp Trp Tyr Ala Pro Gly
305                 310                 315                 320
Glu Trp Met Ile Ser Gly Gln Phe Ser Met Glu Ser Ile Phe Arg Tyr
                325                 330                 335
```

Arg Asp Phe Ile Ser Gln Arg Gln His Ser Thr Leu Ile Thr Leu Asn
340 345 350

Val Ser Lys Lys Phe Phe Gly Ser Thr Leu Gln Leu Ser Asp Phe Thr
355 360 365

Tyr Tyr Asp Leu Thr Gly Lys Gly Trp Phe Ser Arg Phe Ala Ala Asp
370 375 380

Tyr Ala Leu Asn Asp Gln Ile His Leu Met Ala Gly Tyr Asp Trp Phe
385 390 395 400

Ser Ser Lys Gly Ser Gly Ile Phe Asp Arg Tyr Lys Asp Asn Ser Glu
405 410 415

Leu Trp Phe Lys Ala Arg Tyr Ser Phe
420 425

(2) INFORMATION FOR SEQ ID NO:133

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...211

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133

Met Ser Ile Arg Gln Lys Ile Arg Leu Phe His Leu Ser Val Cys Ala
1 5 10 15

Gln Thr His Asp His Leu Ile Glu Ile His Leu Val Cys Ile Glu Phe

20 25 30
Gly Ala Ile Asp Thr Asp Glu Phe Arg Leu Ser Ser His Ala Tyr Thr
35 40 45
Thr Ser Pro Thr His Thr Gly Ala Ile His His Asn Cys Ile Glu Arg
50 55 60
Ser Tyr Gly Arg Tyr Leu Val Thr Phe Gly Gln Glu Arg Asn Glu Leu
65 70 75 80
His His His Ser Arg Pro Asp Arg Asn Ala Glu Val Tyr Arg Phe Pro
85 90 95
Phe Asp Asn Ala Phe His Ser Ile Arg Tyr Glu Ala Phe Arg Pro Ile
100 105 110
Arg Pro Ile Val Cys His Asp Asp His Phe Ile Ala Ile Gly Ser His
115 120 125
Leu Phe Phe Lys Asp Asn Gln Ile Phe Ser Ser Gly Ser Gln Tyr Asp
130 135 140
Asn Tyr Thr Val Ala Cys Phe Val Glu Ser Leu His Asp Arg Glu Gln
145 150 155 160
Arg Ser His Thr His Thr Ala Ser Gly Thr Asn His Cys Ala Asp Leu
165 170 175
Phe Asp Met Arg Thr Leu Ser Gln Arg Thr Tyr His Ile Arg Asp Ile
180 185 190
Val Ala Asp Phe Glu Phe Gly Gln Phe Leu Gly Arg Phe Ala His Gly
195 200 205
Leu Asn His
210

(2) INFORMATION FOR SEQ ID NO:134

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134

```
Met Lys Leu Leu Leu Tyr Leu Leu Leu Val Leu Ser Thr Leu Ser Pro
1               5                   10                  15
Met Tyr Ser Gln Met Leu Phe Ser Glu Asn Leu Thr Met Asn Ile Asp
            20                  25                  30
Ser Thr Lys Thr Ile Gln Gly Thr Ile Leu Pro Val Leu Asp Phe Lys
        35                  40                  45
Thr Glu Lys Glu Asn Val Phe Thr Phe Lys Asn Thr Ala Asn Leu Asn
    50                  55                  60
Leu Leu Ile Lys His Gly Gln Val Ile Asn Leu Ile Asn Lys Leu Glu
65                  70                  75                  80
Phe Ser Thr Tyr Gly Asn Lys Val Thr Val Ser Gly Gly Tyr Val His
                85                  90                  95
Thr Glu Tyr Arg Tyr Leu Leu His His Val Phe Glu Val Tyr Pro Tyr
            100                 105                 110
Val Glu Ser Gln Trp Ala Glu Ser Arg Gly Met Lys Tyr Lys Val Ser
        115                 120                 125
Thr Gly Leu Gln Ser Arg Tyr Arg Leu Val Asn Ser Asp Asn Cys Leu
    130                 135                 140
Met Phe Ala Thr Leu Gly Val Phe Phe Glu Phe Glu Lys Trp Glu Gln
145                 150                 155                 160
Pro Ala Thr Ser Leu Phe Ala Gly Thr Tyr Ala Tyr Ser Arg Ser Ile
                165                 170                 175
Lys Ser His Leu Ser Ile Ser Phe Arg His Arg Leu Gly Glu His Trp
            180                 185                 190
Glu Phe Thr Thr Thr Ala Ile His Gln Gly Lys Pro Asp Ser Tyr Phe
        195                 200                 205
```

```
Lys Lys Ala Arg Phe Gly Gly Ala Ile Asp Leu Lys Tyr His Ile Thr
    210                 215                 220
Pro Thr Ile Gly Ile Arg Gly Ala Tyr Arg Ile Ile Tyr Asp Thr Ala
225                 230                 235                 240
Pro Ile Val Pro Val Arg Lys Asp Tyr Asn Thr Val Asp Val Gly Ile
                245                 250                 255
Asp Ile Ser Phe
            260
```

(2) INFORMATION FOR SEQ ID NO:135

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135

```
Met Lys Thr Asn Arg Arg Tyr Ala Phe Val Leu Pro Leu Leu Leu Leu
1               5                   10                  15
Thr Gly Leu Leu Ala Trp Gly Gln Asp Ser Ser His Gly Ser Asn Thr
            20                  25                  30
Ala Phe Ala Thr Asp Ser Ser Ser Arg Glu Leu Pro Thr Glu Gln Ser
        35                  40                  45
Ala Tyr Arg Ile His Ser Ala Tyr Met Val Gly Gly Gly Gly Ser Ile
```

50 55 60
Thr Arg Asp Thr Tyr Leu Ser Pro Leu Arg Tyr Gly Gly Trp Thr Leu
65 70 75 80
Asn Leu Leu Gly Glu Lys Thr Phe Pro Leu Lys Ala Ser Asp Ser Arg
85 90 95
Trp Met Ile Arg Thr Gly His Glu Leu Asp Phe Ala Leu Met Asp Asn
100 105 110
Pro Ala Asn Asn Ala His Phe Tyr Ser Leu Leu Tyr Asn Gly Ser Ala
115 120 125
Ala Ala Leu Tyr Arg Leu Gly Ala Lys His Leu Arg Ala Ala Trp Met
130 135 140
Asp Asn Leu Arg Leu Ala Phe Gly Pro Gly Leu Glu Ile Gly Leu Gly
145 150 155 160
Gly Ile Tyr Ser Thr Arg Asn Gly Asn Asn Pro Ala Thr Leu Lys Leu
165 170 175
Tyr Thr Asn Ala Ile Ala Gln Ala Ser Ile Gly Tyr Tyr Val Pro Ser
180 185 190
Glu Thr Phe Pro Leu Tyr Phe Arg Leu Leu Ser Gln Ile Asn Leu Phe
195 200 205
Gly Ile Ala Tyr Gly Asn Gly Phe Gly Glu Ser Tyr Tyr Glu Asn Phe
210 215 220
Leu Leu Asn Asn Gly Ile Ala Gly Ser Leu His Phe Thr Tyr Pro Gly
225 230 235 240
Lys Phe Thr Arg Phe Thr Thr Leu Ile Thr Ala Asp Ile Pro Ile Arg
245 250 255
Asn Phe Cys Thr Leu Arg Val Gly Tyr Arg Tyr Ser His Leu Gly Ser
260 265 270
Ser Leu Asn Ala Leu Asp Thr Arg Ile His Ser His Thr Ala Phe Ile
275 280 285
Gly Phe Val Thr Glu Phe Tyr Arg Phe Arg Gly Arg Lys Ala Met Asn
290 295 300
Thr Gly Arg Arg Thr Ser Leu Tyr Tyr His Asp
305 310 315

(2) INFORMATION FOR SEQ ID NO:136

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 776 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136

```
Met Cys Lys Ile Arg Phe Ser Leu Leu Gln Ala Leu Val Val Cys Leu
1               5                   10                  15
Leu Phe Thr Ser Phe Ser Leu Gln Ala Gln Glu Glu Gly Ile Trp Asn
            20                  25                  30
Thr Leu Leu Ala Ile His Lys Thr Glu Lys Ala Val Glu Thr Pro Lys
        35                  40                  45
Lys Val Phe Ala Val Ala Asn Gly Val Leu Tyr Ser Val Gly Lys Glu
    50                  55                  60
Ala Pro His Glu Ala Lys Ile Phe Asp Arg Ile Ser Gly Leu Ser Asp
65                  70                  75                  80
Thr Ser Val Ser Ser Ile Ala Tyr Ser Glu Gln Leu Lys Ser Leu Val
                85                  90                  95
Ile Tyr Tyr Ala Ser Gly Asn Ile Asp Ile Leu Asp Glu Ala Gly Arg
            100                 105                 110
Val Thr Asn Val Pro Ala Leu Lys Asp Asn Ile Asp Leu Ile Asp Lys
        115                 120                 125
Thr Leu Asn Arg Leu Leu Ile Val Gly Asn Arg Ala Tyr Leu Ala Gly
    130                 135                 140
```

```
Ala Glu Cys Asn Pro Gly Asp Ala Arg Val Lys Ala Ile Ala Phe Asp
        435                 440                 445
Asn Lys Gly Asn Leu Trp Gly Thr Leu Gly Ala Val Gly Lys Asn Ile
    450                 455                 460
Phe Met Tyr Asp Pro Gln Ser Ser Thr Trp His Ser Phe Ser Tyr Pro
465                 470                 475                 480
Asp Val Ala Asn Leu Ala Ser Phe Gly Asn Met Ile Ile Leu Pro Asn
                485                 490                 495
Gly Asp Lys Trp Val Asn Ile Leu His Arg Ser Gly Gly Ser Thr Arg
            500                 505                 510
Lys Gly Val Leu Ile Phe Asn Asp Arg Gly Thr Pro Glu Thr Thr Ser
        515                 520                 525
Asp Asp Ser His Leu Tyr Val Glu Gln Phe Val Asn Arg Leu Gly Ala
    530                 535                 540
Ala Ile Gly His Lys Thr Ile Tyr Ala Met Ala Val Asp His Asn Gly
545                 550                 555                 560
Ser Val Trp Met Gly Ser Asp Ile Gly Ile Phe Gly Val Tyr Asn Ala
                565                 570                 575
Ala Gly Val Leu Ser Ser Thr Ser Thr Pro Ile Ala Val Arg Pro Val
            580                 585                 590
Gly Gly Glu Glu Pro Asn Leu Tyr Tyr Val Leu Asp Lys Val Thr Val
        595                 600                 605
Thr Asp Ile Val Val Asp Lys Leu Asn His Lys Trp Val Ala Thr Gln
    610                 615                 620
Gly Thr Gly Leu Tyr Leu Leu Ser Glu Asp Cys Ser Lys Ile Leu Ala
625                 630                 635                 640
Gln Phe Thr Val Glu Asn Ser Pro Leu Leu Ser Asn Asn Ile Leu Ser
                645                 650                 655
Leu Ala Leu Asn Asp Asp Asn Gly Leu Leu Tyr Ile Gly Thr Ala Asp
            660                 665                 670
Gly Leu Met Thr Phe Gln Thr Gly Thr Gly Ser Gly Ser Ala Ser Glu
        675                 680                 685
Leu Asp Gly Val Tyr Val Tyr Pro Asn Pro Leu Arg Pro Glu Tyr Pro
    690                 695                 700
Asp Gly Val Thr Ile Ala Gly Leu Gln Ala Gly Cys Ser Val Lys Ile
705                 710                 715                 720
```

```
Gly Phe Gly Leu Ser Val Leu Asp Val Ala Glu Ala Arg Ile Pro Ala
145                 150                 155                 160
Thr Tyr Ala Lys Gly Thr Lys Val Thr Asp Val Ala Lys Leu Asp Asn
                165                 170                 175
Asp Arg Leu Leu Met Leu Lys Glu Gly Gln Leu Phe Ile Gly Lys Glu
            180                 185                 190
Thr Asp Asn Leu Gln Asp Pro Ala Ala Trp Thr Ala Leu Ser Leu Asn
        195                 200                 205
Leu Pro Met Gly Ser Val Thr Gly Leu Gly Ile Val Gly Glu Asp Ile
    210                 215                 220
Cys Phe Leu Leu Ala Asp Gly Arg Val Tyr Val Ala Ala Asn Gln Ser
225                 230                 235                 240
Phe Glu Pro Glu Leu Leu Leu Ser Ser Ser Ala Asp Ser Arg Leu Tyr
                245                 250                 255
Val Thr Asp Arg Gly Leu Phe Ile Cys Ala Glu Asn Arg Ile Tyr Phe
            260                 265                 270
Ile Glu Lys Gly Arg Lys Thr Thr Gln Phe Pro Ile Ala Asp Val Leu
        275                 280                 285
Gly Val Gly Ala Met Asn Glu Ser Asn Thr Ala Tyr Ile Ala Leu Gly
    290                 295                 300
Glu Glu Gly Leu Ala Ser Leu Leu Leu Ala Glu Gly Ser Thr Ala Glu
305                 310                 315                 320
Ala Met Pro Val Ala Phe Asp Gly Pro Gly Asp Asn Asp Phe Tyr Glu
                325                 330                 335
Met Arg Phe Ser His Gly Arg Leu Tyr Ala Ala Ser Gly Leu Trp Gly
            340                 345                 350
Thr Asn Leu Met Gly His Ala Gly Met Val Lys Leu Tyr Asp Gly Asn
        355                 360                 365
Arg Trp Thr Asn Phe Asp Lys Lys Thr Val Gln Glu Gln Leu Gly Gly
    370                 375                 380
Gly Phe Ser Phe Asn Asp Ala Ile Asp Ile Ala Val Ser Asn Gly Asp
385                 390                 395                 400
Pro Asp His Phe Phe Val Gly Thr Trp Gly Asn Gly Leu Phe Glu Phe
                405                 410                 415
Lys Asp Gly Lys Ala Ile Ala Arg Tyr Ser Gly Asn Glu Thr Ala Ile
            420                 425                 430
```

Thr Asp Thr Thr Gly Arg Leu Leu Tyr Gln Thr Glu Ser Val Thr Thr
725 730 735

Glu Val Lys Trp Asn Ala Arg Gly Ala Asp Gly Asn Arg Val Ala Ser
740 745 750

Gly Val Tyr Ala Val Ala Val Tyr Asp Pro Val Ser Lys Lys Ser Lys
755 760 765

Leu Ile Arg Phe Ala Val Ile Arg
770 775

(2) INFORMATION FOR SEQ ID NO:137

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Porphyromonas gingivalis

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137

Met Arg Phe Gln His Tyr Leu Ile Cys Thr Ala Ala Val Ala Ala Leu
1 5 10 15

Ala Ala Asn Pro Leu Thr Gly Gln Ser Asn Met Thr Leu Glu Glu Cys
20 25 30

Ile Asp Tyr Ala Arg Arg His Ser Ser Ala Val Ala Leu Ser Ala Ala
35 40 45

Glu Leu Glu Gln Ser Lys Ala Asp Tyr Leu Gln Ala Val Gly Asn Phe

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    50                  55                  60
Leu Pro Arg Val Ser Ala Gly Thr Gly Ala Ser Trp Asn Phe Gly Arg
65                  70                  75                  80
Gly Leu Asp Ala Glu Thr Asn Thr Tyr Thr Asp Ile Asn Ser Phe Asn
                85                  90                  95
Asn Ser Tyr Ser Ile His Ala Thr Met Thr Leu Phe Asp Gly Leu Gln
            100                 105                 110
Ser Val Tyr Arg Leu Arg Met Ala His Ala Arg Arg Glu Ala Ser Arg
        115                 120                 125
Leu Ser Val Arg Glu Gln Gln Glu Leu Ala Ala Leu Gly Thr Thr Glu
    130                 135                 140
Ala Tyr Tyr Asp Leu Val Tyr Ala Arg Gln Met Gln Glu Leu Ala Met
145                 150                 155                 160
Gln Lys Tyr Glu Glu Ser Ser Arg Leu His Arg Gln Thr Ala Arg Met
                165                 170                 175
Glu Glu Leu Gly Met Lys Ser Arg Pro Asp Val Leu Glu Met Gln Ser
            180                 185                 190
Arg Met Ala Gly Asp Arg Leu Ala Leu Thr Gln Ala Asp Asn Gln Cys
        195                 200                 205
Ile Ile Ala Leu Ile Arg Leu Lys Glu Lys Met Asn Phe Pro Ile Asp
    210                 215                 220
Asp Glu Leu Val Val Asp Asp Met Pro Ala Asp Ser Leu Ser Ala Asp
225                 230                 235                 240
Met Ala Glu Ser Asp Ser Ser Ala Gly Val Phe Ala Arg Ala Ala His
                245                 250                 255
His His Pro Val Leu Leu Arg Ala Lys Leu Asp Glu Gln Ala Ala Thr
            260                 265                 270
Asp Arg Leu Arg Ala Ala Arg Gly Ala Phe Leu Pro Ser Val Ser Val
        275                 280                 285
Ser Gly Gly Trp Asn Thr Gly Phe Ser Arg Phe Leu Asn Gly Ser Asp
    290                 295                 300
Tyr Thr Pro Phe Ser Glu Gln Phe Arg Asn Arg Arg Gly Glu Tyr Val
305                 310                 315                 320
Ser Leu Asn Leu Ser Ile Pro Ile Phe Ser Gly Phe Ser Leu Val Ser
                325                 330                 335
Leu Arg Gln Ala Arg Ala Gln Arg Arg Ala Ala Ile Val Arg Arg
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                340                 345                 350

Gly Glu Ala Glu Arg Arg Leu Tyr Ser Glu Ile Ala Gln Ala Met Ala
            355                 360                 365
Asp Arg Asp Ala Ala Leu Ala Ser Tyr Arg Gln Ala Lys Glu His Thr
        370                 375                 380
Asp Ala Met Gln Thr Ala Tyr Glu Ala Val Leu Gln Arg Tyr Glu Glu
385                 390                 395                 400
Gly Leu Asn Thr Ala Ile Asp Leu Thr Thr Gln Ala Asn Arg Leu Leu
                405                 410                 415
Asp Ala Arg Val Gln Arg Leu Arg Ala Ala Met Thr Tyr Arg Leu Lys
            420                 425                 430
Cys Lys Leu Ile Ala Tyr Tyr Gly Cys Leu Ser Asp
        435                 440
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